

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: April 24, 2002, 15:26:09 ; Search time 15:01 Seconds  
(without alignments)  
1096.183 Million cell updates/sec

Title: US-09-454-651B-23  
Perfect score: 1149  
Sequence: 1 GLSHFCSGVTHVTKEVKEYA.....LRLVQNOTFWNTT1KQEHEFPDN 216

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 7674552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:  
\* \* \* \* \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1149	100.0	288	2	A45803	B-cell-restricted antigen B7 precursor - human
2	1085	94.4	289	2	G00031	B7 protein - red-C
3	738	64.2	299	2	I46690	CDB80 precursor - r
4	601.5	52.3	321	2	I54766	B-lymphocyte activ
5	561	48.8	309	2	I49503	B-lymphocyte activ
6	182	15.8	329	1	A48754	B7-2 antigen - hum
7	152	13.2	309	2	I49522	gene B7-2 protein
8	140.5	12.2	330	2	I46691	CDB6 precursor - r
9	133.5	11.6	583	2	I39428	alcam - human
10	129	11.2	221	1	Q08E48	BARF1 protein - hu
11	127	11.1	526	2	S70587	butyrophilin precursor
12	122.5	10.7	588	2	JH0206	adhesion molecule
13	122.5	10.7	588	2	A44254	surface glycoprote
14	120.5	10.5	509	2	JCS288	SHP substrate-1 pr
15	120.5	10.5	513	2	JCS289	SHP substrate-1 pr
16	118	10.3	487	2	S65133	butyrophilin - mou
17	116.5	10.1	1088	1	IJX1NL	neural cell adhesi
18	115	10.0	761	1	IJHUNG	neural cell adhesi
19	112.5	9.8	725	2	JE0099	DM-GRASP precursor
20	110.5	9.6	587	2	JH0464	cell surface glyco
21	109	9.5	646	2	I3B049	neural cell adhesi
22	109.5	9.5	853	1	IJBONC	butyrophilin - bov
23	109	9.5	526	1	A37821	protein tyrosine-P
24	109	9.5	2029	1	TDFFLK	protein tyrosine k
25	108	9.4	871	1	I48E96	protein tyrosine k
26	108	9.4	881	1	I48E67	hypothetical prote
27	107.5	9.4	5175	2	T20992	hemicentin precurs
28	107.5	9.4	5198	2	T43390	amalgam protein pr
29	106.5	9.3	333	2	A31923	

## ALIGNMENTS

RESULT 1

A45803 B-cell-restricted antigen B7 precursor - human

N; Alternative names: B-lymphocyte activation antigen B7

C; Species: Homo sapiens (man)

C; Date: 30-Sep-1993 #sequence\_change 30-Sep-1999

C; Accession: I54495; A45003

R; Selvakumar, A.; Freedman, A.S.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.

J. Immunol. 143, 2714-2722, 1992

A; Title: Genomic organization and chromosomal location of the human gene encoding the B7 antigen

A; Reference number: I54495; MUID:92307753

A; Accession: I54495

A; Status: Translated from GB/EMBL/DBJ

A; Molecule type: DNA

A; Residues: 1-288 <RSS>

A; Cross-references: GB:M27533; PID:9184680; PID:AAA36045.1; PID:9306916

A; Cross-references: GB:CD80; CD28LG1; CD28

A; Gene: GDB:CD80

A; Cross-references: GDB:21792; OMIM:112203

A; Map Position: 3q13.3-3q21

A; Introns: 34/1; 140/1; 234/1; 266/1

C; Superfamily: B-lymphocyte restricted antigen B7

C; Keywords: transmembrane protein

F; 1-26/Domain: signal sequence #status predicted <SIG>

F; 248-264/Domain: transmembrane #status predicted <TMM>

Query Match Similarity 100.0%; Score 1149; DB 2; Length 288;  
Best Local Similarity 100.0%; Pred. No. 9 5e-86; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGSVTHVTKEVATLSGCHNVSVEELAQTRIYQKEKKMVLTMMMSGDMNWIPE 60

DB 27 GLSHFCGSVTHVTKEVATLSGCHNVSVEELAQTRIYQKEKKMVLTMMMSGDMNWIPE 86

QY 1 YKNRTIPDITNNLSTIVLALRSPDEGTIVCVLKERYDAFKREHLAETVLISKADFTTPS 120

DB 87 YKNRTIPDITNNLSTIVLALRSPDEGTIVCVLKERYDAFKREHLAETVLISKADFTTPS 146

QY 1 ISDFEIPPSNIRRICSTSGGFEPHLSWLENGBELNAINTIVSQDPETELIAVSSKDF 180

DB 147 ISDFEIPPSNIRRICSTSGGFEPHLSWLENGBELNAINTIVSQDPETELIAVSSKDF 206

QY 181 NMTTNHSMCLIKYGHLYRNQTFNWNTTKQEHFPDN 216

Db	207	NMTNHSFMClikYGLRvnQTFNWNTIKQEHPDN	242	Qy	124	FEIPTSNIRRIICSTSGGPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDFTNMT	183
<b>RESULT 2</b>							
G00031	B7	protein - red-crowned mangabey (fragment)		Db	149	IGHDPNPKRIRSASGGPPEPRIAMDEGEELNAVNTTVQDQLDTESVSSSELDFNWT	208
C;Species:	Cercocebus torquatus (red-crowned mangabey, white-collared mangabey)			Qy	184	TNHISFMCLIKYGHLRVNQTFNWNTIKQE	211
C;Date:	11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999			Db	209	NNESTIVCLIKYGEELSVCQIFPWSPKPQE	236
C;Accession:	G00031			RESULT	4		
R;Villinger, F.J.	submitted to the EMBL Data Library, January 1995					B-lymphocyte activation antigen 7-1 precursor - rat	
A;Status:	preliminary; translated from GB/EMBL/DBJ					C;Species: Rattus norvegicus (Norway rat)	
A;Accession:	G00031					C;Accession: 154766 #sequence_revision 29-May-2000	
A;Molecule number:	GO0217					C;Accession: 154766 #text_change 19-May-2000	
A;Residues:	1-289 <RES>					R;Judge, T.A.; Liu, M.; Christensen, P.J.; Fak, J.J.; Turka, L.A.	
A;Cross-references:	EMBL:019833; PIDN:AAA86700.1; PID:9644783; PIDN:AAA86700.1; PID:9644784					Int. Immunol. 7, 171-178, 1995	
C;Genetics:						A;Title: Cloning the rat homolog of the CD28/CTLA-4-ligand B7-1: structural and functional analysis	
A;Gene:	B7					A;Reference number: 154766; MUID:95232184	
C;Superfamily:	B-lymphocyte restricted antigen B7					A;Accession: 154766	
						A;Status: preliminary; translated from GB/EMBL/DBJ	
						A;Molecule type: mRNA	
						A;Residues: 1-321 <RES>	
						A;Cross references: EMBL:005593; NID:9453381; PIDN:AAA80154.1; PID:9453382	
						C;Superfamily: B-lymphocyte restricted antigen B7	
Query Match	94.4%	Score 1085; DB 2;	Length 289;	Query	Match	52.3%; Score 601.5; DB 2;	Length 321;
Best Local Similarity	95.3%	Pred. No. 1.4e-80;		Best Local Similarity	54.4%; Pred. No. 2.2e-41;		
Matches 205; Conservative		4; Mismatches 6;	Indels 0; Gaps 0;	Matches 112; Conservative 35; Mismatches 58; Indels 1; Gaps 1;			
Qy	2	LSHFCGSVIVHTVKKEVATLSCGHNSVVEELAQTWKEKKVAKLTMISGDMNWIPEY	61	Qy	1	GLSHFCGSVIVHTVKKEVATLSCGHNSVVEELAQTWKEKKVAKLTMISGDMNWIPEY	59
Db	28	LSHFCSGSVIVHTVKKEVATLSCGHNSVVEELAQTWKEKKVAKLTMISGDMNWIPEY	87	Db	31	GLLQITSSGIVEQVSKSVREKAIIKFCSEQSHTRYQKHDMLSYTSGVPEVWP	90
Qy	62	KNRTIDITNNLSIVTLARPSDEGYECVVLKYKEKDAKREHLAEVTLSVKADEFPTPSI	121	Qy	60	EYKNRTIDITNNLSIVTLARPSDGTGTYECVVLKYKEKDAKREHLAEVTLSVKADEFPTP	119
Db	88	KNRTIDITNNLSIVTLARPSDEGYECVVLKYKEKDAKREHLAEVTLSVKADEFPTPSI	147	db	91	KYKNRTVYDANNYPSLQSLGILTSQDGTGTYECVVLKYKEKDAKREHLAEVTLSVKADEFPTP	150
Qy	122	SDFEITSNIRRIICSTSGGPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDFN	181	Qy	120	SISDFEILPTSNIRRICSTSGGPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDFN	179
Db	148	TDFEIDPSNIRRIICSTSGGPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDFN	207	db	151	NITEEGNPNSADIKRITCEASSGFKPRLSWSLENGRELNGINTTISQDPESELYTSSQLD	210
Qy	182	MTTNHSFMClikYGLRvnQTFNWNTIKQEHPDN	216	Qy	180	FNMTRNHSFmLIKYGHLRVNQTFNWNTIKQEHPDN	205
Db	208	MTTNHSFVCLikYGLRvnQTFNWNTPKQEHFPDN	242	Db	211	FNATyDHFIDCFIEYGAHVSQNFIW	236
RESULT	3			RESULT	5		
I46690	CD80 precursor - rabbit			I49503			
C;Species:	Oryctolagus cuniculus (domestic rabbit)			N;Alternate names: MB7-2			
C;Date:	14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999			C;Species: Mus musculus (house mouse)			
A;Accession:	I46690			C;Accession: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999			
A;Molecule type:	mRNA			R;Selvakumar, A.; White, P.C.; Dupont, B.			
A;Residues:	1-39 <ISO>			Immunogenetics 38, 292-295, 1993			
A;Cross-references:	GB:049843; NID:9755096; PIDN:BA08643.1; PID:9755097			A;Title: Genomic organization of the murine B-lymphocyte activation antigen B7			
C;Superfamily:	B-lymphocyte restricted antigen B7			A;Reference number: I49503; MUID:9330789			
				A;Accession: I49503			
Query Match	64.2%	Score 738; DB 2;	Length 299;	Query	Match	64.2%; Score 738; DB 2;	Length 299;
Best Local Similarity	63.9%	Pred. No. 1.8e-52;		Best Local Similarity	63.9%; Pred. No. 1.8e-52;		
Matches 133; Conservative		36; Mismatches 39; Indels 0; Gaps 0;		Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;			
Qy	4	HFFSGSVIVHTVKKEVATLSCGHNSVVEELAQTWKEKKVAKLTMISGDMNWIPEY	63	Qy	4	HFFSGSVIVHTVKKEVATLSCGHNSVVEELAQTWKEKKVAKLTMISGDMNWIPEY	63
Db	29	HSSSGISQVTKSKEMALSCDNNSIDEALARVYRQDQVNLISIISQVYEWPEY	88	Db	29	HSSSGISQVTKSKEMALSCDNNSIDEALARVYRQDQVNLISIISQVYEWPEY	88
Qy	64	RTFPDIINNLSTIVTLARPSDEGYECVVLKYKEKDAKREHLAEVTLSVKADEFPTPSI	123	Qy	64	RTFPDIINNLSTIVTLARPSDEGYECVVLKYKEKDAKREHLAEVTLSVKADEFPTPSI	123
Db	89	RTFPDIINNLSTIVTLARPSDEGYECVVLKYKEKDAKREHLAEVTLSVKADEFPTPSI	148	Db	89	RTFPDIINNLSTIVTLARPSDEGYECVVLKYKEKDAKREHLAEVTLSVKADEFPTPSI	148

R;Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Ueda, T.  
Biochem. Biophys. Res. Commun. 200, 443-449, 1994.

A;Title: Identification of an alternatively spliced form of the murine homologue of B7.  
A;Reference number: I49521; MUID:94220123  
A;Accession: I49521  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-143-238-274, 'R', 279-309 <RE2>  
A;Cross-references: GB:DI6220; NID:950518; PIDN:BA03748.1; PID:994763  
C;Genetics:  
A;Gene: B7  
A;Introns: 37/1; 143/1; 237/1; 275/1  
C;Superfamily: B-lymphocyte restricted antigen B7  
C;Keywords: alternative splicing

Query Match 48 8%; Score 561; DB 2; Length 309;  
Best Local Similarity 50.7%; Pred. No. 3.9e-38; Mismatches 58; Indels 2; Gaps 2;  
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

RESULT 7

Qy 12 VTKKEVATLSCGHNVSVELLAQTRIYQKEKMLTNNMSGDNNIWIPEYKNRTIFTIN 71  
Db 42 LISKSYKDVILPCKRYNSPHEDESDRIYQKHDKVVLSTAGKLUWPKYKNRFLYDTN- 100

Qy 72 NLSIVTLAALRPSDETYECVVKYKEDKFREHLAEVTLSVKADEFPTPSISDFEIPTSNI 131  
Db 101 YFSLLIGLVLSDRDTYSCVYQKFERGTYEKVHIALYKLSIAFEESTPNUTESGNPSAD 160

Qy 132 RRIICSTSGFPPEPHLSWLNNEELNAINNTVSQDPETELYAVSSSKLDFNMNTNHSFMCIL 191  
Db 161 KRITFASGGEPKPRFSLNGRELPGINTTISQDPESELYTTISQDFTNTTRNHTIKCL 220

Qy 192 IKYGLHRVNTENWWTTKQEFPDN 216  
Db 221 IKYDAHVSEDETWKRPPEDE-PDS 244

\* RESULT 6

A48754 B7-2 antigen - human  
B7-2 antigen - human  
A;Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor  
C;Species: Homo sapiens (man)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999

B;Freeman, G.J.; Gruben, J.G.; S39055; 39055  
B;Science 262, 909-911, 1993  
A;Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell prolif  
A;Reference number: A48754; MUID:94053735  
A;Accession: A48754  
A;Molecule type: mRNA  
A;Residues: 1-329 <RE2>  
A;Cross-references: GB:L25259; NID:9416368; PIDN:AA58389.1; PID:9416369  
A;Note: it is uncertain whether Met-1 or Met-7 is the initiator  
R;Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza, C.  
A;Title: B70 antigen is a second ligand for CTLA-4 and CD28.  
A;Reference number: S39055; MUID:94050123  
A;Accession: S39055  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 7-329 <AZU>  
A;Cross-references: GB:U004343; NID:9439838; PIDN:AB003814.1; PID:9439839  
C;Genetics:  
A;Gene: GDB:CD86; CD28LG2  
A;Cross-references: GDB:432597; OMIM:601020  
A;Map position: 3q13.3-3q21  
C;Superfamily: B7-2 antigen  
C;Keywords: glycoprotein

Query Match 15.8%; Score 182; DB 1; Length 329;  
Best Local Similarity 29.0%; Pred. No. 2e-07;

Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;  
Qy 18 EVATLSC ---GHNVSVELLAQTRIYQKEKMLTNNMSGDNNIWIPEYKNRTIFTI 69  
Db 34 ETADLPCOFANSONSOLSELV ---VFWDQDENLVNLNEVYLGEKERFDVSXKMYRTSFD- 89

Qy 70 TNNSIVTLAALRPSDETYECVVKYKEDKFREHLAEVTLSVKADEFPTPSISDFEIPTS 129  
Db 90 SDSWTLRLHNQIKDQKGYQCTIHHKKPTGMIRHQMSNLSEANEQPEI ---VPTPS 145

Qy 130 NIR ---RRIICSTSGFPPEPHLSWLENGBELNAINTV ---SODPETELYAVS 175  
Db 146 NITENWYINLTCSSTHGYPPEPKKNSVL ---LRTKNSTIEYDGIMQKSQDNVTELYDV 200

Qy 176 SKLDF ---NMNTNHSFMCMLIKYGHLRV 199  
Db 201 ISLSVSPDPDVTSNMNTIFCILETDKTRL 227

RESULT 7

I49522 gene B7-2 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #text\_change 23-Jul-1999  
C;Accession: I49522  
R;Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gibben, J.G.; Ng, J.W.; Kim J. Exp. Med. 178, 2185-2192, 1993  
A;Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell A;Reference number: I49522; MUID:9405585  
A;Accession: I49522  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Cross-references: GB:L25606; NID:9432478; PIDN:AAA79770.1; PID:9432479  
C;Genetics:  
A;Gene: B7-2  
C;Superfamily: B7-2 antigen

Query Match 13.2%; Score 152; DB 2; Length 309;  
Best Local Similarity 26%; Pred. No. 4.9e-05; Mismatches 78; Indels 26; Gaps 10;  
Matches 52; Conservative 43; Mismatches 78;

Qy 20 ATLSC ---GHNVSVELLAQTRIYQKEKMLTNNMSGDNNIWIPEYKNRTIFTI 69  
Db 36 AYLPCPCTKAQNISLSELV ---VFWDQDENLVNLNEVYLGEKERFDVSXKMYRTSFD- 89

Qy 70 TNNSIVTLAALRPSDETYECVVKYKEDKFREHLAEVTLSVKADEFPTPSISDFEIP 127  
Db 90 RNNWTLRLHNQIKDQKGYQCTIHHKKPTGMIRHQMSNLSEANEQPEI ---VPTPS 147

Qy 128 TNNSIVTLAALRPSDETYECVVKYKEDKFREHLAEVTLSVKADEFPTPSISDFEIP 182  
Db 148 TGNSGINLTCSTSQGHFKPKAMFLITINSTNEYGDNNOISQDNTELFISNSLSSLSPD 207

Qy 183 -TNHSPCMCLIKYGHLRV 200  
Db 208 GYWHMTVVCVLETESMRIS 226

RESULT 8

I46691 CD86 precursor - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 23-Jul-1999  
C;Accession: I46691  
R;Isono, T.; Seto, A.  
Immunoetics 42, 217-220, 1995  
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole A;Reference number: I46691  
A;Accession: I46691  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA

Residues: 1-330 <ISO>  
Cross-references: GB:D49842; NID:9755098; PIDN:BAA08642.1; PID:g9755099

A; Cross-references: EMBL:VO1555; NID:959074; PIDN:CAA24809-1; PID:91334917  
 R; Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.  
 Nature 310, 207-211, 1984  
 A; Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.  
 A; Reference number: A03794; MUID:84270667  
 A; Contents: annotation; protein coding region  
 C; Subfamily: betacov; homologous genes: -  
 C; Subfamily: betacov; homologous genes: -

ISU LT 9  
 94428  
 can - human  
 Species: Homo sapiens (man)  
 Accession: I39428  
 Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 21-Jul-2000  
 Molecule: mRNA  
 Author: B. Malacko, A.R.; Wang, W.C.;  
 Title: Cloning, mapping, and characterization of activated leukocyte-cell  
 Reference number: I39428; MUID:9527947  
 Accession: I39428  
 Status: preliminary; translated from GB/EMBL/DDBJ  
 Molecule type: mRNA  
 Residues: 1-583 <RES>  
 Cross-references: GB:L38608; NID:9886257; PID:AA59499.1; PID:9886258

Query Match	11.6%	Score	133.5	DB	2	Length	583
Best Local Similarity	24.5%	Pred. No.	0.0034				
Matches	37	Conservative	35	Mismatches	54	Indels	25
Gaps							
59	PEYKRTIDITNNLIVIALRPSDEGYCIVLKKEYKREHIAEVTLUSVKADFPT	118					
	:: :   :: :   :: :   :: :   :: :   :: :   :: :   :: :   :: :						
84	PEYKDR--LNLSNTENYLISNARISDKEFVCMLYT EDVNFEAPITVKV	133					
	:: :   :: :   :: :   :: :   :: :   :: :   :: :   :: :   :: :						
119	PSISDFE---IPTSNIRRI-ICSTSSGGFPWHLNGELNAINNTV-----SFD	166					
	:: :   :: :   :: :   :: :   :: :   :: :   :: :   :: :   :: :						
134	PSKPEIVSKALFLEEQKLKGDCISEDYPGPNITWYRNGKVLPPEGAIVVIIFFKEMD	193					
	:: :   :: :   :: :   :: :   :: :   :: :   :: :   :: :   :: :						
167	PETELYAVSSKLDENMII--TNHSEFMOLIKY	194					
	:: :   :: :   :: :   :: :   :: :   :: :   :: :   :: :   :: :						
194	PVTQLYMTNSTLEYKTTKADIQMPCSVTY	224					

A; Reference number: JH0506; MUID:92030150  
 A; Molecule type: mRNA  
 A; Residues: 1-568 <YAM>  
 A; Cross-references: GB:S63276; NID:9238000; PIDN:AAB20170.1; PID:9238001  
 A; Experimental source: embryo  
 A; Accession: PS270  
 A; Molecular type: protein  
 A; Residues: 34-48 <MAN1>  
 C; Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons  
 C; Keywords: glycoprotein, transmembrane protein  
 F; 1-33/Domain: signal sequence #status predicted <SIG>  
 F; 34-568/Product: adhesion molecule SC1 #status predicted <ADH>  
 F; 500-523/Domain: transmembrane #status predicted <TRA>  
 F; 101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #status  
 A; Map position: 2

Query Match Score 122.5; DB 2; Length 588;  
 Best Local Similarity 25.7%; Pred. No. 0.027; Indels 27; Gaps 8;  
 Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

Qy 59 PEYKNRTIFDTNNLISIVILALRSPDEGYECVVKYERDAFKRHLAETVLSKADFPT 118  
 Db 90 EDYKDR -LSSENNTLISKARISDEKRFVCLMVT-EDDVSEEPVVKV-----FKQ 139  
 Qy 119 PS-----ISDFEIPTSNIRRI -ICSTSGGFPPEHLSWLENG-----EELNAINTTVSQ 165  
 Db 140 PSQPELHQAFD -LETEKLKMLGECVRDSLSPPEGNYTWYKNGRVLQPVEEVVNLRKVE 198  
 Qy 166 DPETELYAVSSKLDFNM T -TNHSPMCLIKY 194  
 Db 199 NRSTGLFTMTSSLQMPTEKDANAKETCIVTY 230

RESULT 13  
 A45254 surface glycoprotein BEN precursor - chicken  
 C; Accession: A45254; S19202  
 C; Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jul-2000  
 C; Accession: A45254; S19202  
 C; Species: Gallus gallus (chicken)  
 F; Pourcel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M.  
 Proc. Natl. Acad. Sci., U.S.A. 89, 5261-5265, 1992  
 A; Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed in  
 A; Reference number: A45254; MUID:92302244  
 A; Accession: A45254  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-568 <POU>  
 A; Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C; Keywords: glycoprotein

Query Match Score 122.5; DB 2; Length 588;  
 Best Local Similarity 25.7%; Pred. No. 0.027; Indels 27; Gaps 8;  
 Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

Qy 59 PEYKNRTIFDTNNLISIVILALRSPDEGYECVVKYERDAFKRHLAETVLSKADFPT 118  
 Db 90 EDYKDR -LSSENNTLISKARISDEKRFVCLMVT-EDDVSEEPVVKV-----FKQ 139  
 Qy 119 PS-----ISDFEIPTSNIRRI -ICSTSGGFPPEHLSWLENG-----EELNAINTTVSQ 165  
 Db 140 PSQPELHQAFD -LETEKLKMLGECVRDSLSPPEGNYTWYKNGRVLQPVEEVVNLRKVE 198  
 Qy 166 DPETELYAVSSKLDFNM T -TNHSPMCLIKY 194  
 Db 199 NRSTGLFTMTSSLQMPTEKDANAKETCIVTY 230

RESULT 14  
 J5288 surface substrate-1 protein, 509 - mouse  
 C; Species: Mus musculus (house mouse)

C; Date: 16-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 20-Jun-2000  
 C; Accession: JCS288  
 R; Yamao, T.; Matczak, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujio, A.; Biochem. Biophys. Res. Commun. 231, 61-67, 1997  
 A; Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization  
 A; Reference number: JC5287; MUID:97223399  
 A; Contents: Brain  
 A; Accession: JCS288  
 A; Molecule type: mRNA  
 A; Residues: 1-509 <YAM>  
 A; Cross-references: DDBJ:D87967; NID:91864012; PIDN:BAA13520.1; PID:91864013  
 C; Comment: This protein is a glycosylated receptor-like protein and plays a role in actions as a docking protein and induce translocation of SHP-2 from the cytosol to the C; Genetics:  
 A; Gene: shps-1  
 A; Map position: 2

Query Match Score 120.5%; DB 2; Length 509;  
 Best Local Similarity 25.9%; Pred. No. 0.032; Indels 39; Gaps 15;  
 Matches 59; Conservative 42; Mismatches 88; Indels 39; Gaps 15;

Qy 3 SHFCGVY----IHTVKEVYEA-----TLSCGHNNVSEEEAQTRIYWK---EKMV 48  
 Db 23 SCFCGTGVTGKELKVQPEKSYSVAAGDSTVLNC--TLSLLPVGPVKWYRGVGSRLLI 79

Qy 49 TMMMSGDNNIWPPEYKRNRTIEDIT -NNU -SIVILALRSPDSEGYECVVKYEDKAFFREH 104  
 Db 80 YSFTEGBH -FPRVTN -VSDATKRNNMDFSRISNTVPEDAGTYYCV -KFQKGPSBPDT 133

Qy 105 L-----AEVPLSVKADEFPTS -ISDFEIPSNIRRICSTSGGFPEP -HLSWLENEL 156  
 Db 134 EIQSGGTEVYVLAQSPPEVGPADRPQKV -NETCKSHGFSPPNITKWFQKQEL 192

Qy 157 NAINTVSDPPTELYAVS -KLDPMTNHSMCILKYCHLRVNQT 202  
 Db 193 HHLETIVNPSGKNVSYNISSTYRVVLSMDVHS -KVICEVAHTLDRS 239

RESULT 15  
 JCS289 SHP substrate-1 protein, 513 - mouse  
 C; Species: Mus musculus (house mouse)  
 C; Date: 16-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 20-Jun-2000  
 C; Accession: JCS289  
 R; Yamao, T.; Matczak, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujio, A.; Biochem. Biophys. Res. Commun. 231, 61-67, 1997  
 A; Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization  
 A; Reference number: JC5287; MUID:97223399  
 A; Contents: Brain  
 A; Accession: JCS289  
 A; Molecule type: mRNA  
 A; Residues: 1-513 <YAM>  
 A; Cross-references: DDBJ:D87968; NID:91864014; PIDN:BAA13521.1; PID:91864015  
 C; Comment: This protein is a glycosylated receptor-like protein and plays a role in actions as a docking protein and induce translocation of SHP-2 from the cytosol to the C; Genetics:  
 A; Gene: shps-1  
 A; Map position: 2

Query Match Score 120.5%; DB 2; Length 513;  
 Best Local Similarity 25.9%; Pred. No. 0.033; Indels 39; Gaps 15;  
 Matches 59; Conservative 42; Mismatches 88; Indels 39; Gaps 15;

Qy 3 SHFCGVY----IHTVKEVYEA-----TLSCGHNNVSEEEAQTRIYWK---EKMV 48  
 Db 23 SCFCGTGVTGKELKVQPEKSYSVAAGDSTVLNC--TLSLLPVGPVKWYRGVGSRLLI 79

Qy 49 TMMMSGDNNIWPPEYKRNRTIEDIT -NNU -SIVILALRSPDSEGYECVVKYEDKAFFREH 104  
 Db 80 YSFTEGBH -FPRVTN -VSDATKRNNMDFSRISNTVPEDAGTYYCV -KFQKGPSBPDT 133

Qy 105 L-----AEVTLVKADFPPTPS-ISDFEIPTSNIRRIICSTSGGFPEP-HLSWLENGEEL 156  
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |  
Db 134 EI0SGGGTEVVYLAKEPSPPEVSEPADRGIPDQKV-NFTCKSIGFSPRNTLKWFKDGEL 192

Qy 157 MAINTIVSQDPETELYAVSS--KLDFNMNTTNISFMCLIKYGHLRVNQT 202  
: : ||| : | | : | | : | | : | | : | | : | | : | | : | | : | | : |  
Db 193 HILETTVNPSPGKNSVNISSSTRVVLNSMDVHS-KVICEVAHTLDRS 239

Search completed: April 24, 2002, 15:31:02  
Job time: 293 sec

Result No.	Score	Query	Match	Length	DB ID	Description
1	114.9	100.0	288	1	CD80_HUMAN	P33681 homo sapien
2	738	64.2	299	1	CD80_RAFT	P42070 orcytolagus
3	561	48.8	306	1	CD80_MOUSE	P00609 mus musculus
4	182	15.8	329	1	CD86_HUMAN	P42081 homo sapien
5	161	14.0	302	1	ICOL_HUMAN	075144 homo sapien
6	152	13.2	309	1	CD86_MOUSE	P42082 mus musculus
7	150.5	13.1	322	1	ICOL_MOUSE	Q9Jhj8 mus musculus
8	140.5	12.2	330	1	CD86_RAFT	P42071 orcytolagus
9	134.5	11.7	583	1	C116_MOUSE	Q61490 mus musculus
10	133.5	11.6	583	1	C116_HUMAN	Q137490 homo sapien
11	129	11.2	221	1	BRFL_EBV	P03228 epstein-bar
12	127	11.1	526	1	BUTY_HUMAN	P01341 homo sapien
13	122.5	10.7	598	1	C116_CHICK	P42292 gallus gallus
14	119	10.4	524	1	BUTY_MOUSE	Q62556 mus musculus
15	116.5	10.1	1088	1	NCAL_XENIA	P16170 xenopus laevis
16	115	10.0	761	1	NCAL_HUMAN	P13592 homo sapien
17	115	10.0	848	1	NCAL_HUMAN	P13591 homo sapien
18	110.5	9.6	321	1	TCB_FLV	P1364 feline leuk
19	109.5	9.5	646	1	MU18_HUMAN	P43121 homo sapien
20	109.5	9.5	853	1	NCAL_BOVIN	F31836 bos taurus
21	109	9.5	526	1	BUTY_BOVIN	P18892 bos taurus
22	109	9.5	2029	1	LAR_DRONE	P16621 drosophila
23	108.5	9.4	365	1	CXAR_MOUSE	P97792 mus musculus
24	106.5	9.3	333	1	AMAL_DRONE	P15364 drosophila
25	106.5	9.3	858	1	NCAL_RAT	P13596 ratius norvegicus
26	105	9.1	319	1	A33_HUMAN	P99795 homo sapien
27	105	9.1	1091	1	NCAL_CHICK	P13590 gallus gallus
28	104	9.1	1092	1	NCA2_XENIA	P36335 xenopus laevis
29	103.5	9.0	725	1	NCAL_MOUSE	P13594 mus musculus
30	103	9.0	1115	1	NCAL_MOUSE	P13595 mus musculus
31	103	9.0	298	1	VEJA_HUMAN	P57087 homo sapien
32	102	8.9	1443	1	NEOL_CHICK	P99610 gallus gallus
33	101.5	8.8	403	1	RAGE_MOUSE	P62151 mus musculus

-!- DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd80.htm".

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CC EMBL; M27533; AAA36045; 1; -;

DR EMBL; M83077; AAA8390; 1; -;

DR EMBL; M83072; AAA8390; 1; JOINED.

EMBL; M83073; AAA8390; 1; JOINED.

DR PIR; A41803; A45803; -;

DR MIM; 112203; -;

DR InterPro; IPR003599; 19.

DR InterPro; IPR003006; 19\_MHC.

DR SMART; SM000409; IG; 1.

DR SMART; SM000410; IG-like; 1.

KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;

Receptor.

SIGNAL 1 34 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.

FT CHAIN 35 288 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 35 242 POTENTIAL.

FT TRANSMEM 243 263 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 264 288 IG-LIKE V-TYPE DOMAIN.

FT DOMAIN 43 123 IG-LIKE C2-TYPE DOMAIN.

FT DISULFID 155 223 POTENTIAL.

FT DISULFID 50 116 POTENTIAL.

FT DISULFID 162 216 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 288 AA; 33048 MW; BA453EE34528BF4 CRC64;

Query Match 100.0%; Score 1149; DB 1; Length 288;

Best Local Similarity 100.0%; Pred. No. 3\_6e-89;

Matches 216; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GLSHFCGSVIIHTKEYKEVALTSGCHNVSVEELAQTTRYWKEKKMVLTMMSGDMMNIWPE 60

Db 27 GLSHFCGSVIIHTKEYKEVALTSGCHNVSVEELAQTTRYWKEKKMVLTMMSGDMMNIWPE 86

Qy 61 YKNRTLFIDTNNSLTVTLALRPSDETYECVVKYKEKDAFKREHLAETVLSKADFPPTS 120

Db 87 YKNRTLFIDTNNSLTVTLALRPSDETYECVVKYKEKDAFKREHLAETVLSKADFPPTS 146

Qy 121 ISDFEIPTSNIRRICSTSGFPPEPHLSWLENGEELNAINTVSDPTELYAVSSKLDF 180

Db 147 ISDFEIPTSNIRRICSTSGFPPEPHLSWLENGEELNAINTVSDPTELYAVSSKLDF 206

Qy 181 NMTTNHSFMCILKYGHLRVNQFWNTIKOEHFPDN 216

Db 207 NMTTNHSFMCILKYGHLRVNQFWNTIKOEHFPDN 242

Qy RESULT 2

CD80\_RABBIT ID CD80\_RABBIT STANDARD; PRT: 299 AA.

~ DCTP207; AC P42070; ~ DTP1195; (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1

DE ANTIGEN).

GN Orctolagus cuniculus (Rabbit).

OS Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.

OC NCBI\_TaxID=9886;

OX RN [11]

RP SEQUENCE FROM N.A.

RC STRAIN=B-J X CHBB; HM;

RX MEDLINE=9536849; PubMed=7642234;

RA ISONO T.; SENO A.;

RT "Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules";

RL Immunogenetics 42:217-220(1995).

CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS RECEPTOR.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.

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CC -!- DR EMBL; D49844; BAA08643; 1; -;

DR InterPro; IPR003599; Ig;

DR InterPro; IPR003006; Ig-MHC.

DR InterPro; IPR003600; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM000409; Ig; 1.

DR SMART; SM000410; Ig-like; 1.

KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;

Receptor.

SIGNAL 1 34 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.

FT CHAIN 35 288 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 35 242 POTENTIAL.

FT TRANSMEM 243 263 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 264 288 IG-LIKE V-TYPE DOMAIN.

FT DOMAIN 43 123 IG-LIKE C2-TYPE DOMAIN.

FT DISULFID 155 223 POTENTIAL.

FT DISULFID 50 116 POTENTIAL.

FT CARBOHYD 162 216 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 288 AA; 33048 MW; BA453EE34528BF4 CRC64;

Query Match 64.2%; Score 738; DB 1; Length 299;

Best Local Similarity 63.9%; Pred. No. 8\_9e-55;

Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

Qy 4 HFCSGVTHVKVKEVALTSGCHNVSVEELAQTTRYWKEKKMVLTMMSGDMMNIWPEYNK 63

Db 29 HFSSG1SQVTKSVKAALSDYNSIDEALARMYIWORDQMVLSIISGVVEWPEYKN 88

Qy 64 RTIEDITNNISLTVTLALRPSDETYECVVKYKEKDAFKREHLAETVLSKADFPPTS 123

Db 89 RTFPD1INNSLMLIALRSKGTTCVVKRNENGSRREHLSVTLSRADFPVPSITD 148

Qy 124 FEIPISNRRIICSTSGFPPEPHLSWLENGEELNAINTVSDPTELYAVSSKLDF 183

Db 149 IGHDPNVTKRIRSASGSFPEPLAMMEDGEELNAVNTVDQDLDTELYSVSELDFNVT 208  
 QY 184 TNHSFMCILKIGHLRVNOTFWNTTQE 211  
 Db 209 NNHISITVCLIKYGELSVSQIFPNSKPQKE 236

RESULT 3  
 CDB0\_MOUSE ID CDB0\_MOUSE STANDARD; PRT; 306 AA.  
 AC Q00609; PRT; 306 AA.  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1  
 DE ANTIGEN) (B7).  
 GN CDB0 OR B7.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Rodentia; Sctiurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RX MEDLINE=91341422; PubMed=1714935;  
 RA Gray G.S., Freeman G.J., Gianni C.D., Lombard D.B., Zhou L.J.,  
 RA White M., Fingeroth J.D., Gibbons J.G., Nadler L.M.;  
 RT "Structure, expression, and T cell costimulatory activity of the  
 murine homologue of the human B lymphocyte activation antigen B7."  
 RL J. Exp. Med. 174:625-631(1991).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RX MEDLINE=93307789; PubMed=7686531;  
 RA Selvakumar A., White P.C., Dupont B.;  
 RT "Genomic organization of the mouse B-lymphocyte activation antigen  
 B7."  
 RL Immunogenetics 38:292-295 (1993).

CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T  
 CC LYMPHOCYTES ACTIVATION T CELL PROLIFERATION AND CYTOKINE  
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD80 OR CTLA-4 TO THIS  
 CC RECEPTOR.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA  
 CC MALIGNANCIES, STIMULATED MONOCYTES AND NONCIRCULATING B-CELL

CC -1- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-  
 CC ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND  
 CC IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST ACTIVATION.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; X60958; CAA43291.1;  
 DR EMBL; L12589; AA37240.1; ALT\_SEO.  
 DR EMBL; L12585; AA37240.1;  
 DR EMBL; L12586; AA37240.1; JOINED.  
 DR EMBL; L12587; AA37240.1; JOINED.  
 DR EMBL; L12588; AA37240.1; JOINED.  
 DR PIR; SJ7291; S17291.  
 DR MGD; MGI:101775; Cd80.  
 DR InterPro; IPR003559; Ig.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003600; Ig\_like.  
 DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; Ig; 1.  
 DR SMART; SM00410; Ig like; 1.  
 KW Immuno-globulin domain; T-cell; Glycoprotein; Signal; Transmembrane;  
 KW Receptor.  
 FT SIGNAL 1 37  
 FT CHAIN 38 246  
 FT DOMAIN 38 246  
 FT TRANSMEM 247 268  
 FT DOMAIN 269 306  
 FT DOMAIN 47 126  
 FT DOMAIN 158 226  
 FT DISULFID 227 246  
 FT DISULFID 54 119  
 FT CARBOHYD 165 210  
 FT CARBOHYD 93 93  
 FT CARBOHYD 99 99  
 FT CARBOHYD 149 149  
 FT CARBOHYD 189 189  
 FT CARBOHYD 210 210  
 FT CARBOHYD 214 214  
 SQ SEQUENCE 306 AA; 34589 MW; 10RADE931B8AC62 CRC64;

Query Match 48.8%; Score 561; DB 1; Length 306;  
 Best Local Similarity 50.7%; Pred. No. 5.8e-40;  
 Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

QY 1.2 VTREVKVEATLSCGHNVSYELLQTRIVQKEKKVMTMSGMDNNIPWBYKNTFIDTN 71  
 Db 42 LSRSVKDVLVLPCKRNPSPHEDDESDR1WQHDKVVLVSVIAGKLKVWBEYKNFTLYDT- 100

QY 72 NLSIVTIALRPSDEGTYECVVLYEKDAFKREHLAETLSSVKADEFPTPSISDFEPTSNI 131  
 Db 101 TYSLLIGLVLSRGTYECVVQKKGRTYEVKHALVKSIAKDFSTNITEGGNPASD 160

QY 132 RRICSTSGGFPEPHLSWLENGFELNAINTVYSDQPELEYAVSSKLDENMTTNHSFMCL 191  
 Db 161 KRITCAFSGFPKPRESWLNGRELPGINTTSQDPESELYTSSQLDENTRNHTKCL 220

QY 192 IKYGLHRVNQTFWNNTTROEHFDN 216  
 Db 221 IKYDAHVSEDFTEWKPPEDP-PDS 244

RESULT 4  
 CDB0\_HUMAN STANDARD; PRT; 329 AA.  
 ID CDB0\_HUMAN STANDARD;  
 ID CDB0\_HUMAN STANDARD;  
 AC P42081; Q13655;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2  
 DE ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.2) (B70) (FUN-1) (B063).  
 GN CD86 OR CD2LG2.  
 OS Homo sapiens (Human).  
 OC Euksaryota; Metzoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TAXID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94053735; PubMed=7694363;  
 RA Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,  
 RA Restivo V.A. Jr., Lombard L.A., Gray G.S., Nadler L.M.,  
 RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T  
 cell proliferation";  
 RL Science 262:909-911(1993).  
 RN [2]  
 RP SEQUENCE OF 7-329 FROM N.A.  
 RX MEDLINE=94050123; PubMed=7694153;  
 RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,  
 RA Laiier L.L., Somoza C.;  
 RT "B70 antigen is a second ligand for CTLA-4 and CD28";  
 RL Nature 366:76-79(1993).

[3]	RN SEQUENCE OF 7-329 FROM N.A.	FT CARBOHYD 146 N-LINKED (GLCNAC. . .) (POTENTIAL);
RP TISSUE-Foreskin;	FT CARBOHYD 154 N-LINKED (GLCNAC. . .) (POTENTIAL);	
RC MEDLINE=95331831; PubMed=7411777;	FT CARBOHYD 177 N-LINKED (GLCNAC. . .) (POTENTIAL);	
RA Jellis C.L., Wang S.S., Rennert P., Borriello F., Sharpe A.H.,	FT CARBOHYD 192 N-LINKED (GLCNAC. . .) (POTENTIAL);	
RA Green N.R., Gray G.S.,	FT CARBOHYD 213 N-LINKED (GLCNAC. . .) (POTENTIAL);	
RT "Genomic organization of the gene coding for the costimulatory human	FT CONFLICT 27 K -> E (IN REF. 3).	
RT B-lymphocyte antigen B7-2 (CD86).";	SQ SEQUENCE 329 AA; 37696 MW; 65D4F3826889CF7D CRC64;	
RL Immunogenetics 42:85-89 (1995).		
RN [4]		
RP CHARACTERIZATION.		Query Match 15.8%; Score 182; DB 1; Length 329;
RX MEDLINE=95088403; PubMed=7527824;		Best Local Similarity 29.0%; Pred. No. 3.2-e-08;
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,		Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;
RA RAKA K., Ito D., Azuma M.;		
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL.",		
RL J. Immunol. 154:97-105 (1995).		
RN [5]		
RP IDENTIFICATION AS CD86.		Db 34 ETADLPCQFANSQNSLSELVY--EVWQDNVLNEVYLGKEKFKSVHVKMGRSFDF- 89
RX MEDLINE=94348060; PubMed=7520767;		Db 70 TNNLSTVILALRPSDGTYECVLYKVEKDAFKREHIAEVTLVKADEPTPSISDFEPTS 129
RA Nadler L.M., Watasa H., Tedder T.F.;		Db 90 SDSWTLRLHNQLRDKGLYQCLIHKKPTGMIRHMOMSELSVLANESQPEI---VPIS 145
RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and activated B lymphocytes is the CD86 differentiation antigen.",		
RL Blood 84:1402-1407 (1994).		
CC FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.		
- - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		Db 130 NIR---RITCSTSGFPEP-HLSWLENGEELNNTV-----SQDPETELYAVS 175
- - TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND CC		Db 146 NITENVYINJCSSJHGYPEPKMSVL---LRTRNSTIEYDGIMOKSQDNVNTELVDVS 200
CC		
CC		Db 176 SKLDF--NMNTTNHFSMCLIKYGHLYV 199
CC		Db 201 ISLSVSPFDVTISNMTCIFCLETDKTRL 227
RESULT 5		
ICOL_HUMAN		
ID ICOL_HUMAN STANDARD; PRT; 302 AA.		
AC Q9HJ8;		
DT 07114; Q9HJ8; Q9HJ8; Q9HJ8;		
DT 15-JUL-1999 (Rel. 38, Created)		
DT 20-AUG-2001 (Rel. 40, Last sequence update)		
DT 20-AUG-2001 (Rel. 40, Last annotation update)		
DE ICOS LIGAND PRECURSOR (B7 HOMOLOG 2) (B7-H2) (B7-LIKE PROTEIN GL50)		
DE (B7-RELATED PROTEIN 1) (B7RP-1).		
DE ICOSL OR B7H2 OR B7RP1 OR KIAA053.		
GN Homo sapiens (Human).		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TaxID=9606;		
RN [1]		
RP SEQUENCE FROM N.A. (ISOFORM 1).		
RC TISSUE=Dendritic cell;		
RC PubMed=11023515;		
RX Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.; RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds ICOS";		
RT ICOS";		
RT Blood 96:2808-2813 (2000).		
RN [2]		
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.		
RC TISSUE=Peripheral blood lymphocytes;		
RC PubMed=11007762;		
RX Yoshihaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K., Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H., Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;		
RT "Characterization of a new human B7-related protein: B7RP-1 is the ligand to the co-stimulatory protein ICOS.";		
RT Int. Immunol. 12:1439-1447 (2000).		
RL [3]		
RN SEQUENCE FROM N.A. (ISOFORM 2).		
RC TISSUE=Leukocyte;		
RC PubMed=20126021; PubMed=10657606;		
RX Ling V., Wu P.W., Farmer H.F., Bean K.M., Spaulding V., Fouser L.A., Leonard J.P., Hunter S.E., Zoller R., Thomas J.L., Miyashiro J.S., Jacobs K.A., Collins M.;		
RA "Identification of GL50, a novel B7-like protein that functionally binds to ICOS receptor.";		
RT RL J. Immunol. 164:1653-1657 (2000).		
RN		

RP	SEQUENCE FROM N.A. TISSUE=Brain;	CARBOHYD	225	225	N-LINKED (GLCNAC. . .) (POTENTIAL).
RC	PUBMED=9734811; PubMed=9734811;	VARSPPLIC	300	302	GHV->ESWNLLLIS (IN ISOFORM 2).
RA	Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 5;169-176(1998). [5]	SEQUENCE	302 AA;	33349 MW;	64794AE21B5E34A CRC64;
RP	SEQUENCE FROM N.A. (ISOFORM 2).	Query Match	14.0%	Score 161;	DB 1; Length 302;
RA	"G150 molecules and uses therefor.";	Best Local Similarity	26.4%;	Pred. No. 1.6e-06;	
RT	Patent number WO0121796, 29-MAR-2001.	Matches	57;	Mismatches	95; Indels 28; Gaps 8;
RL	-1- FUNCTION: LIGAND FOR THE T-CELL SPECIFIC CELL SURFACE RECEPTOR ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).	Qy	14 KEVKEV ---ATLSCG-HNVSVEELAQTRIWQ-KEKKVLT---MSGDMNIWPEYKN 63		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).	Db	23 KEVRANVGSVDVELSCAQPEGSREDLNDDVYVWNTSEKTVYHIPONSSLENVDSRYRN 82		
CC	-1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.	Qy	64 RTIFED----ITNLNSIVTIALRPSDECTYECVVKYKEVDAFKREHLAEVTLSVKADEPTP 119		
CC	-1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART, MARMOW, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE, SPLEEN, COLON, Ovary, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES, LYMPH NODES, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN SPLEEN, THYMUS AND SPLEEN.	Db	83 RALMSPAGMLRQDFSLSLFNLNTVTPQDEKFHCLVLVS-QSLGQEVLSVTILVAANSVP 141		
CC	-1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.	Qy	120 SISDFEPLTSNURILLCSTSGGFPEPHLSWLENGEELNAINTTVVSOPETE-----L 171		
CC	-1- SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.	Db	:I : VVSAPHSPSQDLETFETTSINGYPRPNVYWINRKTD-----NSLQLQALQNLTFLNMNRGL 196		
CC	-1- SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.	Qy	172 YAVSSKLDFDNMTTNHSMSCLIKYGHFLRVNQNPENWNT 207		
CC	-1- SUBFAMILY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.	Db	142 YDVVSVLRARTPSVNGCCTENVLQQLNTYGSQT 232		
CC	-1- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITION 300 ONWARD FOR AN UNKNOWN REASON.	RESULT	6		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	ID	CD86_MOUSE	STANDARD;	PRT; 309 AA.
CC	CC - INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.	AC	P42082;		
CC	-1- SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.	DT	01-NOV-1995 (Rel. 32, Created)		
CC	-1- SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.	DT	01-NOV-1995 (Rel. 32, Last sequence update)		
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.	DT	20-AUG-2001 (Rel. 40, Last annotation update)		
CC	-1- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITION 300 ONWARD FOR AN UNKNOWN REASON.	DE	T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2 ANTIGEN) (EARLY T CELL COSTIMULATORY MOLECULE-1) (ETC-1).		
CC	CC -	GN	GN186.		
CC	CC -	OS	Os musculus (Mouse).		
CC	CC -	OC	OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Sciurognathii; Muridae; Murinae; Mus.		
CC	CC -	OX	OX NEBI_TAXID=10090;		
CC	CC -	RN	RN SEQUENCE FROM N.A.		
CC	CC -	RX	RX MEDLINE=94005585; PubMed=7504059;		
CC	CC -	RA	RA Freeman G.J., Borriello F., Hoddes R.J., Reiser H., Gibben J.G., Ng J.W., Kim J., Goldberg J.M., Lombard J.A., Wang S., Gray G.S., Nadler L.M., Hatchcock K., Laszlo G.,		
CC	CC -	RA	RA Wang S., Gray G.S., Nadler L.M., Hatchcock K., Laszlo G.,		
CC	CC -	RT	RT "Murine B7-2, an alternative CTLA4 counter receptor that costimulates T cell proliferation and interleukin 2 production.";		
CC	CC -	RL	RL J. Exp. Med. 178:2185-2192(1993).		
CC	CC -	RN	RN [2]		
CC	CC -	RP	RP SEQUENCE FROM N.A.		
CC	CC -	RX	RX MEDLINE=94230971; PubMed=7499829;		
CC	CC -	RA	RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;		
CC	CC -	RT	RT "Differential expression of alternate mb7-2 transcripts.";		
CC	CC -	RL	RL J. Immunol. 155:5490-5497(1995).		
CC	CC -	RN	RN [3]		
CC	CC -	RP	RP SEQUENCE OF 7-309 FROM N.A.		
CC	CC -	RX	RX MEDLINE=94230971; PubMed=7513726;		
CC	CC -	RA	RA Chen C., Gault A., Shen L., Nabavi N.;		
CC	CC -	RT	RT "Molecular cloning and expression of early T cell costimulatory molecule-1 and its characterization as B7-2 molecule.";		
CC	CC -	RL	RL J. Immunol. 152:4939-4936(1994).		
CC	CC -	CC	CC - FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.		
CC	CC -	CC	CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	CC -	CC	CC - TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.		
CC	CC -	CC	CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.		
FT	FT	ICOS LIGAND.			
FT	FT	POTENTIAL.			
FT	FT	EXTRACELLULAR			
FT	FT	(POTENTIAL).			
FT	FT	CYTOSOLIC			
FT	FT	(POTENTIAL).			
FT	FT	V-TYPE DOMAIN.			
FT	FT	IG-LIKE C2-TYPE DOMAIN.			
FT	FT	POTENTIAL.			
FT	FT	POTENTIAL.			
FT	FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			



- 1 - TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S PATCHES (MOSTLY IN THE FOLLICLES). LOWER LEVELS IN MANY NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG, SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF ISOFORM 2 IS RESTRICTED TO HEART, SPLEN AND KIDNEY.

- 1 - DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPoIESIS; IN THE YOLK SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT 14.5 DPC

- 1 - SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.

- 1 - SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.

- 1 - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG SUBFAMILY.

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MMBL1	AF216747; AAF05149.1; .
MMBL2	AF199027; AAF04738.1; .
MMBL3	XJ100541; CAC3663.1; .
MMBL4	AX100593; CAC1646.1; .
MMBL5	AF394451; AAK77544.1; .
IGGD1	MGI:1354701; Igos1.
InteretroPro	IPRO03599; Ig.
InterPro	IPRO03599; Ig.
InterPro	IPRO03600; Ig-like.
InterProPro	IPRO03006; Ig_MHC.
Fam1	PFO0047; Ig; 1.
SMART	SM00409; Ig; 1.
SMART	SM00410; Ig-like; 1.
- Cell activation; Immune response; Glycoprotein; Transmembrane; Multigene family;	

Alternative splicing.		BY SIMILARITY.
SIGNAL	1	46
SIGNAL	47	322
SIGNAL	47	277
TRANSMEM	278	298
TRANSMEM	299	322
DOMAIN	55	145
DOMAIN	178	250
DOMAIN	31	38
DOMAIN	289	292
DISULFID	62	138
DISULFID	195	242

ZJSLID	NAME	IN	OUT	LINK	TYPE	REF
183	ZARBOYD	743	741	N-LINKED	(GLCNAC, . . .)	(POTENTIAL).
184	ZARBOYD	71	120	N-LINKED	(GLCNAC, . . .)	(POTENTIAL).
185	ZARBOYD	120	163	N-LINKED	(GLCNAC, . . .)	(POTENTIAL).
186	ZARBOYD	163	200	N-LINKED	(GLCNAC, . . .)	(POTENTIAL).
187	ZARBOYD	200	213	N-LINKED	(GLCNAC, . . .)	(POTENTIAL).
188	ZARBOYD	213	252	N-LINKED	(GLCNAC, . . .)	(POTENTIAL).
189	ZARBOYD	252	265	N-LINKED	(GLCNAC, . . .)	(POTENTIAL).
190	ZARBOYD	265	322	N-LINKED	(GLCNAC, . . .)	(POTENTIAL).
191	PARSPLIC	321	322	HA -> TWADPVQDYLIPRLMSPLKTRGLP	(1)	ISOPORT 2).
237	CONFLICT	237	339960	MW;	R -> H (IN REF. 4 AND 5; CAC36464).	55CCBA1AD12E7E CRC64;
322	AA:					

Db	93	PYKSPGPIVQDSSYKNGHLSLSDMKGSFLYLKNTVPQDTQEFTRVY-FMATAEVLK	150
QY	105	LAE-VTILSVKADEFPTP--SISDFEELPTSNIIRRIGCSTSGGFPEPHISWLLENGEELNAIN	160
Db	151	LEEEFVYRLRVAANESPVVISDSSSPQQE-RTYCHSKNGTYPEFVLYWI-NITDNLNSL	208
QY	161	TTVSQDP---ETELYAVSSKLDFENNMTNHSPMLCKIYGHLYRN-----QTFNWNTTK	209
Db	209	TALQNNTVYLNLGLYDXVISTLRPLWTSRGDVLCVENVALHONITSISQAESPTGNNTK	268
RESULT	8		
CD86_RABBIT		STANDARD;	PRT;
ID	CD86_RABBIT		330 AA.
AC	P42071;		
DT	01 - NOV - 1995	(Rel. 32)	Created)
DT	01 - NOV - 1995	(Rel. 32)	Last sequence update)
DT	01 - OCT - 1996	(Rel. 34)	Last annotation update)
DE	B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR		ACTIVATION B7-2
DE	ANTIGEN).		
GN	CD86		
OS	Oryctolagus cuniculus (Rabbit)		
OC	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;		

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OC  
OX NCBL-TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=B/J X CHB/RM;  
RX MEDLINE=953369849; PubMed=7642234;  
RA Isono T., Seto A.;  
RT Cloning and sequencing of the rabbit gene encoding T-cell  
costimulatory molecules;  
RL Immunogenetics 2:217-220(1995).  
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL  
CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION. BY  
CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY  
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,  
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T  
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.  
CC  
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CC ch) or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)

FT	CARBOHYD	192	192	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	213	213	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQ	SEQUENCE	330 AA;	37142 MW;	935CD65C57E3EE1 CRC64;	
Query Match		12.28:	Score 140.5; DB 1;	Length 330;	
Best Local Similarity	27.48%; Pred. No. 9.4e-05;				
Matches	60; Conservative	34; Mismatches	84; Indels	41; Gaps	12;
QY	18	EYATLSCGH-NYSVEELAQTTRIYQKEREKKMVLTTM --- SGIMNITPDEYKNTTIDITN - 71			
Db	34	KTADLPCCOPTNSQSRSLSLEVYWDQERLYLFLGREKDPDVDEKYIGTSFEDOESW	93		
QY	72	NLSIVILALRPSDEGTYECVVIKYEKDAFKRHAEVTLSYKADEFPTPSISFEIPHSNI	131		
Db	94	NLQLHNVQIK-DKGIVQCFVHARGKGLVPTYQMNSELSTLAFNQPEIT --- LISNI	147		
QY	132	RR --- LICSTGGFPBPFLPHSLLNGEELNTPNTH --- SODPETLY -- AVSS 176			
Db	148	TRNSAINLTCSVQGYPEPKMKFF --- VLKTENATEYDGTYTEKSDDNVTLGlyNTSISG	203		
QY	177	KLDF - NMTTNHSMCLIKYGHLRVNOTEWNNTKQEHFP	214		
Db	204	SITFSSDIRNATIYCVL --- QTESTEVYSQ-HFP	233		
RESULT	9				
C166_MOUSE					
TD	C166_MOUSE		STANDARD;	PRT;	583 AA.
AC	Q61490-070136;				
DR	01-NOV-1997 (Rel. 35, Created)				
DR	15-JUL-1999 (Rel. 38, Last sequence update)				
DR	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE)				
DE	(ALCAM) (DM-GRASP PROTEIN).				
OS	Mus musculus (Mouse).				
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Muridae; Murinae; Mus.				
RN	[1]				
RN	NCBI_TAXID=10090;				
RP	SEQUENCE FROM N_A.				
RC	STRAIN=NFS;				
RX	MEDLINE=R9753242; PubMed=9209500;				
RA	Bajirath J., D'Eglio M., Whitney G.S., Palmer D.,				
RA	Kobarg J.J., Starling G.C., Siadak A.W., Aruffo A.;				
RA	Characterization of mouse ALCAM (CD166); the CD6 binding domain is conserved in different homologs and mediates cross-species binding.";				
RI	Eur. J. Immunol. 27:1469-1478(1997).				
RI	SEQUENCE OF 227-583 FROM N_A.				
RC	STRAIN=BALB/C; TISSUE=Brain;				
RX	Medline=9437608; PubMed=809660;				
RA	Kanki J.-P., Chang S., Kuvada J.Y.				
RT	"The molecular cloning and characterization of potential chick DM-GRASP homologs in chicken and mouse."				
RL	J. Neurobiol. 25:831-845(1994).				
CC	-!- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF THE NERVOUS SYSTEM.				
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN				
CC	-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 3 C2-LIKE AND 2 V-LIKE DOMAINS.				
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CC	or send an email to license@isb-sib.ch).				
CC	CC DR EMBL; I95030; AAC06342.1; -.				
CC	CC DR MGII; MGII:131266; AAA37528.1; -.				
CC	CC DR InterPro; IPRE003599; Ig.				
CC	CC DR InterPro; IPRO0006; Ig_MHC.				
CC	CC DR InterPro; IP003600; Ig_Like.				
CC	CC DR SMART; SM00419; Ig; 3.				
CC	CC DR PROSITE; PS00290; Ig_MHC; FALSE_NEG.				
CC	CC KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.				
FT	FT SIGNAL	1	27		
FT	FT CHIRIN	28	583		
FT	FT DOMAIN	28	528		
FT	FT TRANSMEM	528	549		
FT	FT DOMAIN	550	583		
FT	FT DOMAIN	263	321		
FT	FT DOMAIN	347	399		
FT	FT DOMAIN	428	492		
FT	FT DISULFID	43	113		
FT	FT DISULFID	157	220		
FT	FT DISULFID	270	313		
FT	FT DISULFID	354	435		
FT	FT DISULFID	435	485		
FT	FT CARBOHYD	95	95		
FT	FT CARBOHYD	167	167		
FT	FT CARBOHYD	265	265		
FT	FT CARBOHYD	306	306		
FT	FT CARBOHYD	361	361		
FT	FT CARBOHYD	457	457		
FT	FT CARBOHYD	480	480		
FT	FT CARBOHYD	499	499		
FT	FT CONFLICT	232	232		
FT	FT CONFLICT	454	454		
SQ	SEQUENCE	583 AA;	65161 MW;	E7BAFF8FC48F9489 CRC64;	
Query	Match	11.7%	Score 134.5; DB 1; Length 583;		
Best	Local	Similarity	25.2%; Pred. No. 0.0061;		
Matches	38;	Conservative	34; Mismatches	54;	Indels 25; Gaps 7;
QY	59	PEYKNRTIFDTINNLSTVILALRPSDEGTTCVVLKEYDKAFKREHLAEVTLSVKADFT	118		
Db	84	PEYKDR - LSLSENVTLSIANAKISDEKFVCMVLTV - EDNFYFEAPTIVKV --- FKQ	133		
QY	119	PSISDFR --- IPTSNIRRI - ICSTSGGFPPPHLSSWLENGBELNATNTVS --- OD	166		
Db	134	PSKPEIVNKAPFLETDLKLKGDC1SRSYDPGNITWYRNGKVLQPVEGEAVLFKEID	193		
QY	167	PETELYAVSSKLDNFNTNH --- SFMCLIKY	194		
Db	194	PGTQLYTTSLEYKTRSDIQMPFTCSVTY	224		
RESULT	10				
C166_HUMAN					
ID	C166_HUMAN		STANDARD;	PRT;	583 AA.
AC	Q13740; O60892;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DE	CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE)				
DE	(ALCAM), ALCAM, ALCAM OR MEMD.				
GN	Homo sapiens (Human).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
CC	NCBI_TAXID=9606;				
RN	[1]				
RP	SEQUENCE FROM N_A.				

MDLINE=95279947; PubMed=7760007;	FT DISULFID 4.3 113 POTENTIAL.
Bowen M.A., Patel D.D., Li X., Modrell B., Malacko A.R., Wang W.-C., Margrath H., Neubauer M., Pesando J.M., Francke U., Haynes B.F.; Aruffo A.; "Cloning, mapping, and characterization of activated leukocyte-cell adhesion molecule (ALCAM), a CD6 ligand.," J. Exp. Med. 181:2213-2220(1995). [2]	FT DISULFID 2.0 220 POTENTIAL.
SEQUENCE OF 2-583 FROM N A. MEDLINS=98161527; PubMed=502422;	FT DISULFID 3.13 313 POTENTIAL.
Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J., van Kooij Y., Bloemers H.P., Swart G.W.; "MEMD, a new cell adhesion molecule in metastasizing human melanoma cell lines, is identical to ALCAM (activated leukocyte cell adhesion molecule).," Am. J. Pathol. 152:805-813(1998). [3]	FT DISULFID 3.92 392 POTENTIAL.
CDD-BINDING DOMAINS. MEDLINS=9620463; PubMed=3823162;	FT DISULFID 4.35 485 POTENTIAL.
Skonier J.E., Bowen M.A., Emswiler J., Aruffo A., Bajorath J.; "Recognition of diverse proteins by members of the immunoglobulin superfamily: delineation of the receptor binding site in the human CD6 ligand ALCAM," Biochemistry 35:12287-12291(1996). [4]	FT CARBOHYD 9.1 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
3D-STRUCTURE MODELING OF 28-133. MEDLINS=96060095; PubMed=8520490;	FT CARBOHYD 9.5 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
Bajorath J., Bowen M.A., Aruffo A.; "Molecular model of the N-terminal receptor-binding domain of the human CD6 ligand ALCAM," Protein Sci. 4:1644-1647(1995). [-] FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN NEURITE EXTENSION NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF THE NERVOUS SYSTEM.	FT CARBOHYD 1.67 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
- - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS C2 LIKE AND 2 V-LIKE DOMAINS. [-] DATABASE: NAME=PROW; NOTE=CD guide cb166 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd166.htm".	FT CARBOHYD 2.65 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
EMBL; L38608; AAB59499.1; EMBL; Y10183; CAA71256.1; PDB; 1KIC; 03-APR-96. PDB; 601662; _-	FT CARBOHYD 3.06 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
InterPro; IPR003599; Ig_MHC. InterPro; IPR003006; Ig_MHC. InterPro; IPR003600; Ig_like. Pfam; PF00047; ig_5. SMART; SM00499; Ig_2. SMART; SM00410; Ig_like_2. PROSITE; PS00290; Ig_MHC; FALSE_NEG. Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; 3D-structure; Polymorphism.	FT CARBOHYD 3.61 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
SIGNAL 1 27 DOMAIN 28 583 DOMAIN 28 527 POTENTIAL. TRANSMEM DOMAIN 5.28 549 EXTRACELLULAR (POTENTIAL).	FT CARBOHYD 4.57 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
TRANSMEM DOMAIN 5.50 583 CYTOPLASMIC (POTENTIAL).	FT CARBOHYD 4.80 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
DOMAIN 3.16 120 DOMAIN 34 399 DOMAIN 3.42 428 DOMAIN 3.49 492 DOMAIN 3.47 477 DOMAIN 3.48 488 DOMAIN 3.49 499 DOMAIN 3.50 500 DOMAIN 3.51 511 DOMAIN 3.52 522 DOMAIN 3.53 533 DOMAIN 3.54 544 DOMAIN 3.55 555 DOMAIN 3.56 566 DOMAIN 3.57 577 DOMAIN 3.58 588 DOMAIN 3.59 599 DOMAIN 3.60 600 DOMAIN 3.61 611 DOMAIN 3.62 622 DOMAIN 3.63 633 DOMAIN 3.64 644 DOMAIN 3.65 655 DOMAIN 3.66 666 DOMAIN 3.67 677 DOMAIN 3.68 688 DOMAIN 3.69 699 DOMAIN 3.70 700 DOMAIN 3.71 711 DOMAIN 3.72 722 DOMAIN 3.73 733 DOMAIN 3.74 744 DOMAIN 3.75 755 DOMAIN 3.76 766 DOMAIN 3.77 777 DOMAIN 3.78 788 DOMAIN 3.79 799 DOMAIN 3.80 800 DOMAIN 3.81 811 DOMAIN 3.82 822 DOMAIN 3.83 833 DOMAIN 3.84 844 DOMAIN 3.85 855 DOMAIN 3.86 866 DOMAIN 3.87 877 DOMAIN 3.88 888 DOMAIN 3.89 899 DOMAIN 3.90 900 DOMAIN 3.91 911 DOMAIN 3.92 922 DOMAIN 3.93 933 DOMAIN 3.94 944 DOMAIN 3.95 955 DOMAIN 3.96 966 DOMAIN 3.97 977 DOMAIN 3.98 988 DOMAIN 3.99 999 DOMAIN 3.10 1000 DOMAIN 3.11 1111 DOMAIN 3.12 1222 DOMAIN 3.13 1333 DOMAIN 3.14 1444 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CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to license@isb-sib.ch).

CC	InterPro; IPR003006; Ig-MHC.
CC	InterPro; IPR003596; Ig-V.
DR	InterPro; IPR003877; SFRY.
DR	Pfan; PF00044; Ig-1.
DR	Pfan; PF00622; SFRY; 1.
DR	SMART; SM00436; IgV.
DR	SMART; SM00449; SFRY; 1.
KW	Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
SQ	SEQUENCE 221 AA; 24471 MW; C5A2AD1EA28758E CRC64;
Query Match	Score 129; DB 1; Length 221;
Best Local Similarity	27.0%
Matches 43; Conservative 25; Mismatches 47; Indels 44; Gaps 8;	Query 18 EYATLSCGHNSVVEELAQTRIYWQK-----EKKAVALTMNSGDMNIWPE 60 Db 19 QAVTAFLGERVTLTS-----YWRVSLGPEIEVSWEFLGPGEQEVQVIGRMHHDV-IFIE 71 Qy 61 YKMRITFDI--TNNLSTIVILALRPSDEGTYCIVVLYKEKDFKREHLAEV--TLSV-- 112 Db 72 WPERGFEDIHRASNTTFLVUTANISHDGNYLCRMKGTEVTKOEHLSVVKPLTLSVHS 131 Qy 113 -KADEFPTPSISDEPIPSNIRRIICSTGGFPPEPHLSWL 150 Db 132 ERSQFP-----DEFSLT-----VTCVNAAFFPHYQWL 159
RESULT 12	RESULTS FROM N.A.
BUTY_HUMAN	STANDARD; PRT; 526 AA.
ID	AC Q13410; RQ11NOV1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE	BTUROPHILIN PRECURSOR (BT).
GN	BTN1A1 OR BTN.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	[1] NCBI_TaxID=9606;
RN	RSPN
RP	SEQUENCE FROM N.A.
RC	TISSUE-Breast;
RX	MEDLINE=96201696; PubMed=8611614;
RA	Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.; "Cloning and sequence analysis of human butyrophilin reveals a potential receptor function.", Biochim. Biophys. Acta 1306:1-4 (1996).
RT	- FUNCTION: MAY ACT AS A SPECIFIC MEMBRANE ASSOCIATED RECEPTOR FOR THE ASSOCIATION OF CITOPLASMIC DROPLETS WITH THE APICAL PLAMA MEMBRANE (BY SIMILARITY).
CC	- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE (BY SIMILARITY).
CC	- SIMILARITY: BELONGS TO THE BTN/MOG SUBFAMILY.
CC	- V-LIKE DOMAIN. BELONGS TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).
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DR	MIM: 601610; AAC50489.1; -
DR	InterPro; IPR003879; Butyroph-DUF-C.
DR	InterPro; IPR001870; Gamma_carboxylise.
DR	EMBL; U39576; AAC50489.1; -
DR	SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.
DR	TISSUE=Bursa of fabricius;
RC	MEDLINE=92302224; PubMed=1608932;

Pourquier O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;  
 RT "BEN," a surface glycoprotein of the immunoglobulin superfamily, is  
 expressed in a variety of developing systems.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).  
 [4]

RN POSSIBLE FUNCTION: RRP  
 RX MEDLINE=92211411; PubMed=1313497;  
 RA Pourquier O., Hallonet M.E.R., le Douarin N.M.;  
 RT "Association of BEN glycoprotein expression with climbing fiber  
 axogenesis in the avian cerebellum.";  
 RL J. Neurosci. 12:1548-1557(1992).  
 CC -I- POSITION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING  
 FIBER AXONOGNOSIS. SUPPORTS NEURITE EXTENSION.

CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -I- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS  
 WITHIN THE SPINAL CORD; IT IS LOCALIZED TO AXONS IN THE DORSAL  
 FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN  
 EPITHELIUM, MENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH  
 DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS  
 OF BEN.

CC -I- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC  
 CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 3 C2-LIKE AND 2 V-LIKE DOMAINS.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to license@isb-sib.ch).

CC -I- CDR EMBL; S63276; ABB20170.1; .  
 DR EMBL; M76678; AAA48602.1; .  
 DR EMBL; X64301; CAA45579.1; .  
 DR HSSP; Q13740; IKGJC.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003600; Ig\_like.  
 DR SMART; SM00409; Ig; 3.  
 DR SMART; SM00410; Ig\_like; 2.  
 DR PROSITE; PS00290; Ig\_MHC; FALSE\_NEG.  
 KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;  
 KW Signal.

FT SIGNAL 1 33 CD166 ANTIGEN. POTENTIAL.  
 FT CHAIN 34 588 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 34 532 POTENTIAL.  
 FT TRANSMEM 533 538 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 554 588  
 FT DOMAIN 42 126 IG-LIKE V-TYPE DOMAIN 1.  
 FT DOMAIN 156 233 IG-LIKE V-TYPE DOMAIN 2.  
 FT DOMAIN 269 326 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DOMAIN 352 404 IG-LIKE C2-TYPE DOMAIN 2.  
 FT DOMAIN 433 497 IG-LIKE C2-TYPE DOMAIN 3.  
 FT DISULFID 49 119 POTENTIAL.  
 FT DISULFID 163 226 POTENTIAL.  
 FT DISULFID 276 319 POTENTIAL.  
 FT DISULFID 359 397 POTENTIAL.  
 FT DISULFID 440 490 POTENTIAL.  
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 485 485 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 504 504 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 2 10 MEPPAAAR -> EPPSRP (IN REF. 3).  
 FT CONFLICT 25 25 A -> S (IN REF. 3).  
 FT CONFLICT 112 113 SD -> RH (IN REF. 3).

FT CONFLICT 329 329 A -> T (IN REF. 2).  
 FT CONFLICT 401 402 LQ -> HK (IN REF. 2).  
 SQ SEQUENCE 588 AA; 65726 MW; 2488612B0164531E CRC64;

Query Match 10.7%; Score 122.5; DB 1; Length 588;  
 Best Local Similarity 25.8%; Pred. No. 0.0062;  
 Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

Qy 59 PEYNARTIFDTNNLSTVIALRPSDEGTVCVVKYERDAFKRPHLAEVTLISKADFPT 118  
 Db 90 PDYKDR-LSLSENTPLTSKKNARI-SDEGKMLVY-EDDVSEEPVVKY-EDDVSEEPVVKY-EDDVSEEPVVKY-FKQ 139

Qy 119 PS-----ISDFEPISTSLLRRI-ICSTGGFPPEHPSWLENG-----EELNAINTVSQ 165

Qy 140 PSQPETLHQADF-LTEKLMGECVRDSYPEGNVNTWYKNGRVLQPVVEVVVNLRKVE 198

Qy 166 DPETELYAVSSSKLDFNM-----TNHSFMCILKY 194

Db 140 NRSTGLFTMTSSLQYMPTEKDNAKFTCIVY 230

Db 199 NRSTGLFTMTSSLQYMPTEKDNAKFTCIVY 230

RESULT 14  
 BUTY\_MOUSE STANDARD; PRT; 524 AA.

ID BUTY\_MOUSE STANDARD;  
 AC Q62556; P97392;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

DB BUTYROPHILIN PRECURSOR (BP).

GN BTN1AL OR BTN N.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=129; TISSUE=Mammary gland;  
 RX MEDLINE=97148936; PubMed=8905761;  
 RA Oggi S.L., Komaragiri M.V.S., Mather I.H.;  
 RT "Structural organization and mammary-specific expression of the  
 RT butyrophilin gene.";  
 RT Mamm. Genome 7:900-905 (1996).  
 RL RN [2]

RP SEQUENCE OF 39-487 FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=96125722; PubMed=8541302;  
 RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;  
 RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin  
 specifically associates with a 150-kDa protein of mammary epithelial  
 cells and milk fat globule membrane.";  
 RL Blochim. Biophys. Acta 1245:285-292 (1995).  
 CC -I- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT  
 CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATE RECEPTOR FOR THE  
 CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA  
 CC MEMBRANE (BY SIMILARITY).  
 CC -I- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.  
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -I- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN  
 CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.  
 CC -I- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF  
 CC PREGNANCY AND IS MAXIMAL DURING LACTATION.  
 CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 1  
 CC V-LIKE DOMAIN. BELONGS TO THE BN/MOG SUBFAMILY.  
 CC -I- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).  
 CC -I- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN  
 CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.  
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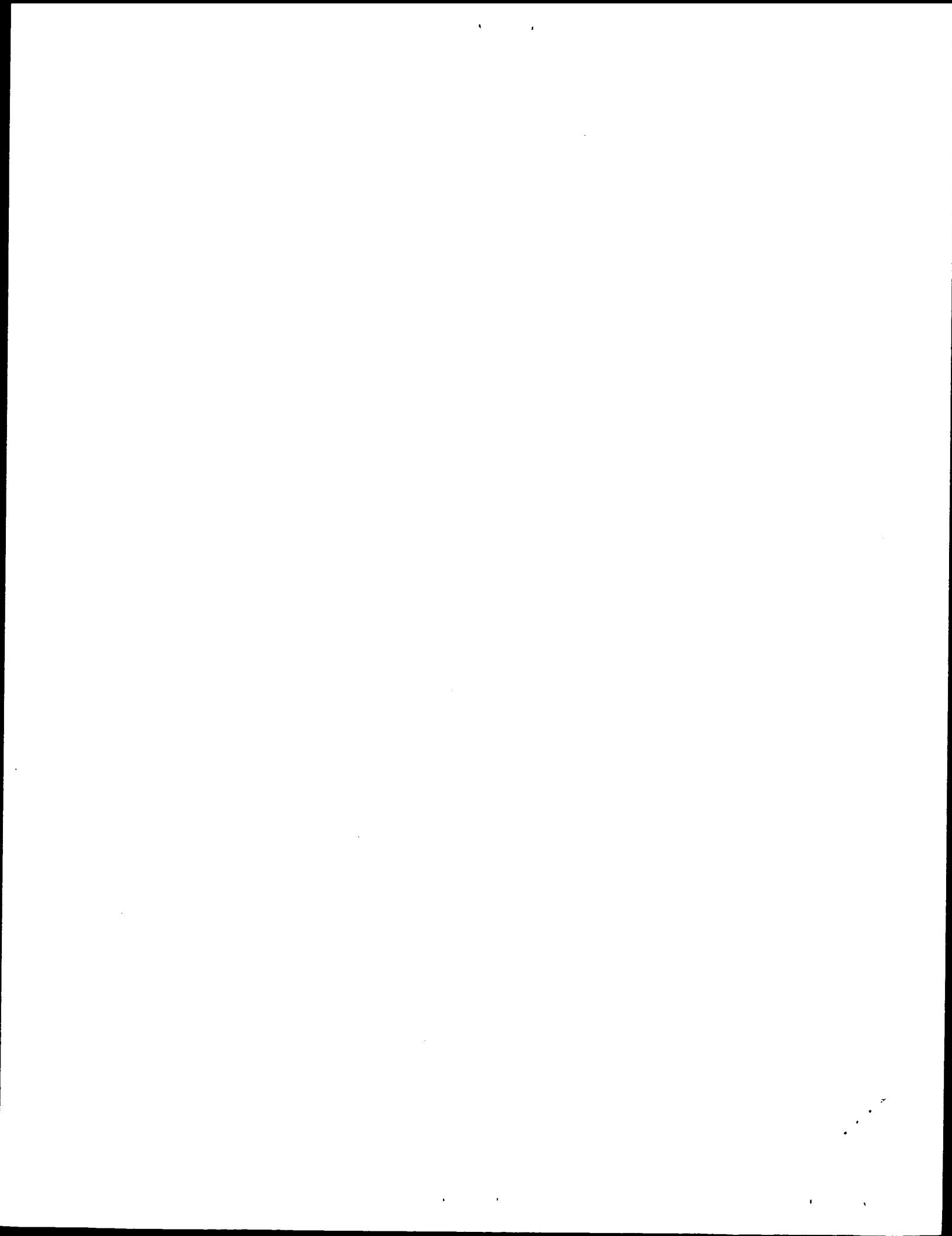
Query Match	
EMBL; S80642;	AA51034_1;
EMBL; S80642;	AA51034_1;
MGD; MGI:103118;	Bnt1al.
InterPro; IPR013879;	Butyroph_DUF_C.
InterPro; IPR01870;	Gamma_carboxylase.
InterPro; IPR01870;	Ig_MHC.
InterPro; IPR01870;	Ig_v.
InterPro; IPR01877;	SPRY.
Pfam; PF00047;	Ig_1.
Pfam; PF00622;	SPRY; 1.
SMART; SM00406;	IGV; 1.
SMART; SM00449;	SPRY; 1.
TRANSMEMBRANE;	Glycoprotein; Immunoglobulin domain; Signal.
SIGNAL;	Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
CHAIN	1
DOMAIN	27
TRANSMEM	248
DOMAIN	269
CARBOHYD	56
CARBOHYD	216
CONFILCT	46
CONFILCT	117
CONFILCT	191
CONFILCT	210
CONFILCT	363
CONFILCT	408
CONFILCT	413
CONFILCT	420
CONFILCT	492
SEQUENCE	524 AA;
	58406 MW;
	10.4%; Score 119; DB 1;
	Length 524;
	33394DE2C7704480 CRC64;

RA	Krieg P.A., Sakaguchi D.S., Kintner C.R.;
RT	"Primary structure and developmental expression of a large cytoplasmic domain form of Xenopus laevis neural cell adhesion molecule (NCAM).";
RT	Nucleic Acids Res. 17:10321-10335(1989).
RL	- - FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC.
CC	- - ALTERNATIVE LOCATION: TYPE I MEMBRANE PROTEIN
CC	- - ALTERNATIVE PRODUCTS: THREE DIFFERENT TISSUE-SPECIFIC FORMS OF NCAM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	- - TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PREMATURE NEURAL TISSUE.
CC	- - DEVELOPMENTAL STAGE: THE mRNA ENCODING THIS LD-NCAM IS THE MAJOR TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING EARLY NEURAL DEVELOPMENT.
CC	- - SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC	- - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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DR	EMBL; M255996; AAA49909.1; -.
DR	PIR; S09600; IJXNL.
DR	HSSP; P56276; 1T1KL.
DR	InterPro; IPR001777; FN_III.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003598; Ig_c2.
DR	Pfam; PF00041; fn3_2.
DR	Pfam; PF00047; ig_5.
DR	SMART; SM00060; FN3_2.
DR	SMART; SM00408; IgC2_5.
DR	Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
KW	immunoglobulin domain; Alternative splicing; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 1088
FT	NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	CYTOSLIC (POTENTIAL).
FT	IG-LIKE C2-TYPE DOMAIN 1.
FT	IG-LIKE C2-TYPE DOMAIN 2.
FT	IG-LIKE C2-TYPE DOMAIN 3.
FT	IG-LIKE C2-TYPE DOMAIN 4.
FT	IG-LIKE C2-TYPE DOMAIN 5.
FT	FIBRONECTIN TYPE-III 1.
FT	FIBRONECTIN TYPE-III 2.
FT	HEPARIN-BINDING (POTENTIAL).
FT	HEPARIN-BINDING (POTENTIAL).
FT	PROBABLE.
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MISSING ('TISOFORN N-CAM 140').
FT	6.22738B5503FEB83 CRC64.
FT	SEQUENCE 1088 AA; 117778 MW;
FT	SEQUENCE 1088 AA; 117778 MW;

Query Match	Score	Length
Best Local Similarity	10.1%	1088
Best Local Matches	24.0%	1
Conservative	0.042	0
Pred. No.	0	0
Nodes	47	0
Misses	58	0
Nodes	47	0

QY 18 EVATLSCGHINVSEBELAQTRIYQKEKKMVLTTMSGDMNIWPEVKNRTLFDTNNLSIVI 77  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
\* Db 130 EDAVITICDVSSSIPSI----TTRHKGRDVI----- FKKDVRFLANNYQI 173  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
QY 78 LAIRPSDEGTYYCVLKYEKDAFKREHIAEVTLISVKADFPPTSPSISDFEI---PTSNIRR- 133  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 174 RGIKTKDEGTYRC----BGRILARGEINYKDIQTVNVP-PTIQARQLRVNATANMAES 227  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
QY 134 -IICSTSGGFPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDFN---MTTNH 186  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 228 VVLSCDADGPDPETSWLKKGEP-----EDGE-----EKISFNEDQSEMTIH 271  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Search completed: April 24, 2002, 15:33:55  
Job time: 191 sec



Database :	SPREMBL_17:*			
1:	sp_archea:*			
2:	sp_bacteria:*			
3:	sp_fungi:*			
4:	sp_human:*			
5:	sp_invertebrate:*			
6:	sp_mammal:*			
7:	sp_minic:*			
8:	sp_organelle:*			
9:	sp_phage:*			
10:	sp_plant:*			
11:	sp_rodent:*			
12:	sp_virus:*			
13:	sp_vertebrate:*			
14:	sp_unclassified:*			
Pred.	No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES				
Result No.	Score	Query Match	Length	DB ID
1	1118	97.3	288	6 Q9GMZ9
2	1100	95.7	288	6 Q9GMZ9
3	1085	94.4	288	6 Q9BDN9
4	1085	94.4	289	6 Q9B347
5	764	66.5	230	6 Q9N2I3
6	762.5	66.4	288	6 Q9TT70
7	762.5	66.4	297	6 Q9BE99
8	761	66.2	229	6 Q9TT71
9	743	64.7	292	6 002758
10	743	64.7	292	6 09GMZ8
11	719	62.6	304	6 Q9IQX1
12	717.5	62.4	296	6 Q96A05
13	705	61.4	235	6 Q9NQ8
14	705	61.4	235	6 Q9N0T0
15	603.5	52.5	321	11 Q35187
16	602	52.4	290	11 Q62680
17	601.5	52.3	321	11 Q62624
18	596	51.9	321	11 Q55202
19	560	48.7	306	11 Q9R1z9

Run on:	April 24, 2002, 15:30:24 ; Search time 23.39 Seconds (without alignments) 1350.783 Million cell updates/sec
Title:	US-09-454-651B-23
Perfect score:	1149
Sequence:	1 GLSHFCSGYTHVTKVEYKA.....LRYNOTENWNTIKQEHPDN 216
Scoring table:	BLOSUM62
Gap cost:	10.0 , Gapext 0.5
Searched:	473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters:	473505
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%	
Maximum Match 0%	
Listing first 45 summaries	

## ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	288 AA.
077684	ID 077684			
	AC 077684;			
	DT .01-NOV-1998 (TREMBLrel. 08, Created)			
	DT .01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
	DT .01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
	DE B7 PROTEIN.			
	GN B7.			
	OS Macaca nemestrina (Pig-tailed macaque).			
	OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi;			
	OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
	OC Cercopithecinae; Macaca.			
	NCBI_TaxID=9545;			
	RN [1]			
	RP SEQUENCE FROM N.A.			
	RA Kraus G., Hnatyssyn J.H.;			
	RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.			
	CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.			
	CC DR AF070519; AAC31555..1; -.			
	DR InterPro; IPR003599; Ig.			
	DR InterPro; IPR003600; Ig-like.			
	DR Pfam; PF00047; Ig; 1.			
	DR SMART; SM000409; Ig; 1.			
	SQ SEQUENCE 288 AA; 33131 MW; 76BBC4283959AB79 CRC04;			
	Query Match 97.3%; Score 1118; DB 6; Length 288;			
	Best Local Similarity 97.7%; Pred. No. 3.e-93; Mismatches 1; Indels 0; Gaps 0;			
QY	2 LSHFCSGVHYTKKEVKVEYATLSCGHNNVSEELAQTRIYWQEKKMYLTMMMSGDMNIWPEY 61			
Db	28 LSHFCSGVHYTKKEVKVEYATLSCGHNNVSEELAQTRIYWQEKKMYLTMMMSGDMNIWPEY 87			
QY	62 KNRTRIDITNNLSIVIALRPSDEGTIECVVLYKEKDAFKREHLAEVTLSSVKADFPPI 121			
Db	88 KNRTIDITNNLSIVIALRPSDEGTIECVVLYKEKDAFKREHLAEVTLSSVKADFPPI 147			

Q9gmz9 felis silve  
Q61332 mus musculu  
Q9xex6 felis silve  
Q9gmz7 felis silve  
Q9ttf1 canis famili  
Q42404 gallus gallus  
Q9tf2 canis famili  
Q9bdn2 cercopithec  
Q9bdn4 macaca mulu  
Q9pab9 papio anubis  
Q9bab8 cercopibus  
Q9g123 bos taurus  
Q35551 rattus norvegicus  
Q02838 sus scrofa  
Q9hd18 homo sapien  
Q9nrq1 homo sapien  
Q9nzq7 homo sapien  
Q9ep73 mus musculus  
Q64381 mus musculus  
Q61238 mus musculus  
Q9j18 mus musculus  
Q9bxr1 homo sapien  
Q46651 orctolagus canis  
P97710 rattus norvegicus  
Q9qw15 rattus norvegicus

077684 macaca mulu  
092499 macaca mulu  
Q9bdn6 cercopibus  
Q28347 cercopithecus  
Q9n2i3 sus scrofa  
Q9ttf0 sus scrofa  
Q9be99 sus scrofa  
Q9ttf1 sus scrofa  
Q02758 felis silve  
Q9tqz8 canis famili  
Q46405 bos taurus  
Q9tqs8 canis famili  
Q9n0t0 canis famili  
Q35187 rattus norvegicus  
Q62680 rattus norvegicus  
Q62624 rattus norvegicus  
Q55202 rattus norvegicus  
Q9rlz9 mus musculus

QY	122	SDFEIPTSNIRRITCSTSGGFPEPHLSWLENGEELNAINTVSDQPETELYAVSSKLDNF	181
Db	148	TDFEIPPSNIRRITCSTSGGFPEPHLSWLENGEELNAINTVSDQPETELYAVSSKLDNF	207
QY	182	MTTNHSFMCLIKYGHLYRNQTFNWNTPKQEHFPDN	216
Db	208	MTTNHSFMCLIKYGHLYRNQTFNWNTPKQEHFPDN	242
RESULT	2		
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	AC	Q28499;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
	DE	DE	
	DE	B7 PROTEIN (CD80 PROTEIN PRECURSOR).	
	GN	GN	
	OS	Cercocetus torquatus atys (Red-crowned mangabey) (Sooty mangabey).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	
	OC	Cercopitheciinae; Cercopithecidae; Cercopithecus.	
	OX		
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.; "Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas Ligand and co-stimulatory molecules.", Immunogenetics 0:0(2001). EMBL: AF344839; AAC37535.1; -.	
	RN	SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;	
QY	2		
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	RX	TISSUE=BLOOD;	
	RA	Medline=96003435; PubMed=7561102;	
	RT	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", J. Immunol. 155:3946-3954 (1995).	
	RT	Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules.", Immunogenetics 0:0(2001). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	RL	EMBL: U19840; AAA86706.1; -.	
	RP	InterPro: IPR003599; Ig.	
	RA	InterPro: IPR003600; Ig-like.	
	CC	InterPro: IPR003006; Ig_MHC.	
	CC	PFAM: PF00047; Ig; Ig_MHC.	
	DR	SMART: SMART; SMART0409; Ig; Ig-like; 1.	
	DR	SMART: SMART0410; Ig; Ig-like; 1.	
	KW	Signal.	
	FT	1 26 POTENTIAL.	
	SQ	SEQUENCE 288 AA; 33141 MW; E70BEA4006C7A609 CRC64;	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
	AC	Q28347;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
	GN	Cercocetus torquatus (red-crowned mangabey).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	TISSUE=BLOOD;	
	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
	AC	Q28347;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
	GN	Cercocetus torquatus (red-crowned mangabey).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
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	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
	AC	Q28347;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
	GN	Cercocetus torquatus (red-crowned mangabey).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	TISSUE=BLOOD;	
	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
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	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
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	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
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	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
	AC	Q28347;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
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	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	TISSUE=BLOOD;	
	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
	AC	Q28347;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
	GN	Cercocetus torquatus (red-crowned mangabey).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	TISSUE=BLOOD;	
	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
	AC	Q28347;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
	GN	Cercocetus torquatus (red-crowned mangabey).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	TISSUE=BLOOD;	
	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
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	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
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	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	TISSUE=BLOOD;	
	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
	AC	Q28347;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
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	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	TISSUE=BLOOD;	
	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
	AC	Q28347;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
	GN	Cercocetus torquatus (red-crowned mangabey).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
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	RN	[1]	
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	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
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	AC	Q28347;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
	GN	Cercocetus torquatus (red-crowned mangabey).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	TISSUE=BLOOD;	
	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	
QY	2		
	Query Match	95.7%; Score 1100; DB 6; Length 288;	
	Best Local Similarity	96.3%; Fred. No. 1.4e-91; Indels 0; Gaps 0;	
	Matches	207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
	Q28347	PRELIMINARY;	PRT; 289 AA.
	AC	Q28347;	
	DT	01-NOV-1996 (TREMBLrel. 01, Created)	
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DE	DE	
	DE	B7 PROTEIN (FRAGMENT).	
	GN	Cercocetus torquatus (red-crowned mangabey).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Cercopithecidae; Cercopithecus.	
	OC	NCBI_TAXID=9530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	TISSUE=BLOOD;	
	RA	Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.", Immunol. 155:3946-3954 (1995). - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
	DR	InterPro: IPR003600; Ig-like.	









DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE B7.1.

GN Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI\_TaxID:10116;

RN [1]

RN [RN]

RP SEQUENCE FROM N. A.

RC STRAIN=FISCHER;

RA Widdegen B., Visse E., Sjogren H.O.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN

EMBL;

DR AF010465; AAB6351.1; -.

DR InterPro; IPR00599; Ig.

DR InterPro; IPR003600; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; Ig; 1.

DR SMART; SM00410; Ig-like; 1.

DR SMART; SM00411; Ig-like; 1.

DR SMART; SM00412; Ig-like; 1.

DR SMART; SM00413; Ig-like; 1.

DR SMART; SM00414; Ig-like; 1.

DR SMART; SM00415; Ig-like; 1.

DR SMART; SM00416; Ig-like; 1.

DR SMART; SM00417; Ig-like; 1.

DR SMART; SM00418; Ig-like; 1.

DR SMART; SM00419; Ig-like; 1.

DR SMART; SM00420; Ig-like; 1.

DR SMART; SM00421; Ig-like; 1.

DR SMART; SM00422; Ig-like; 1.

DR SMART; SM00423; Ig-like; 1.

DR SMART; SM00424; Ig-like; 1.

DR SMART; SM00425; Ig-like; 1.

DR SMART; SM00426; Ig-like; 1.

DR SMART; SM00427; Ig-like; 1.

DR SMART; SM00428; Ig-like; 1.

DR SMART; SM00429; Ig-like; 1.

DR SMART; SM00430; Ig-like; 1.

DR SMART; SM00431; Ig-like; 1.

DR SMART; SM00432; Ig-like; 1.

DR SMART; SM00433; Ig-like; 1.

DR SMART; SM00434; Ig-like; 1.

DR SMART; SM00435; Ig-like; 1.

DR SMART; SM00436; Ig-like; 1.

DR SMART; SM00437; Ig-like; 1.

DR SMART; SM00438; Ig-like; 1.

DR SMART; SM00439; Ig-like; 1.

DR SMART; SM00440; Ig-like; 1.

DR SMART; SM00441; Ig-like; 1.

DR SMART; SM00442; Ig-like; 1.

DR SMART; SM00443; Ig-like; 1.

DR SMART; SM00444; Ig-like; 1.

DR SMART; SM00445; Ig-like; 1.

DR SMART; SM00446; Ig-like; 1.

DR SMART; SM00447; Ig-like; 1.

DR SMART; SM00448; Ig-like; 1.

DR SMART; SM00449; Ig-like; 1.

DR SMART; SM00450; Ig-like; 1.

DR SMART; SM00451; Ig-like; 1.

DR SMART; SM00452; Ig-like; 1.

DR SMART; SM00453; Ig-like; 1.

DR SMART; SM00454; Ig-like; 1.

DR SMART; SM00455; Ig-like; 1.

DR SMART; SM00456; Ig-like; 1.

DR SMART; SM00457; Ig-like; 1.

DR SMART; SM00458; Ig-like; 1.

DR SMART; SM00459; Ig-like; 1.

DR SMART; SM00460; Ig-like; 1.

DR SMART; SM00461; Ig-like; 1.

DR SMART; SM00462; Ig-like; 1.

DR SMART; SM00463; Ig-like; 1.

DR SMART; SM00464; Ig-like; 1.

DR SMART; SM00465; Ig-like; 1.

DR SMART; SM00466; Ig-like; 1.

DR SMART; SM00467; Ig-like; 1.

DR SMART; SM00468; Ig-like; 1.

DR SMART; SM00469; Ig-like; 1.

DR SMART; SM00470; Ig-like; 1.

Qy 52.5%; Score 603.5; DB 11; Length 321;

Best Local Similarity 54.9%; Pred. No. 1-2e-45; Gaps 1;

Matches 113; Conservative 34; Mismatches 58; Indels 1; Gaps 1;

Db 1 GLSHFCSGVI-HVTKEYKEVATLSCGHNVSYVEELAQTRIYQKEKKMVLTMMSGDMNIWP 59

Db 31 GFQISSGIVGVSKYREKALLSCDKFCSEEQSIRIYQKHDKMVLSTISGYPEVWP 90

Qy 60 EYKNPTEFDITNNLISIYLAIRPSDGEYCVLYKEKDARKREHTAEVTLVKADEPTP 119

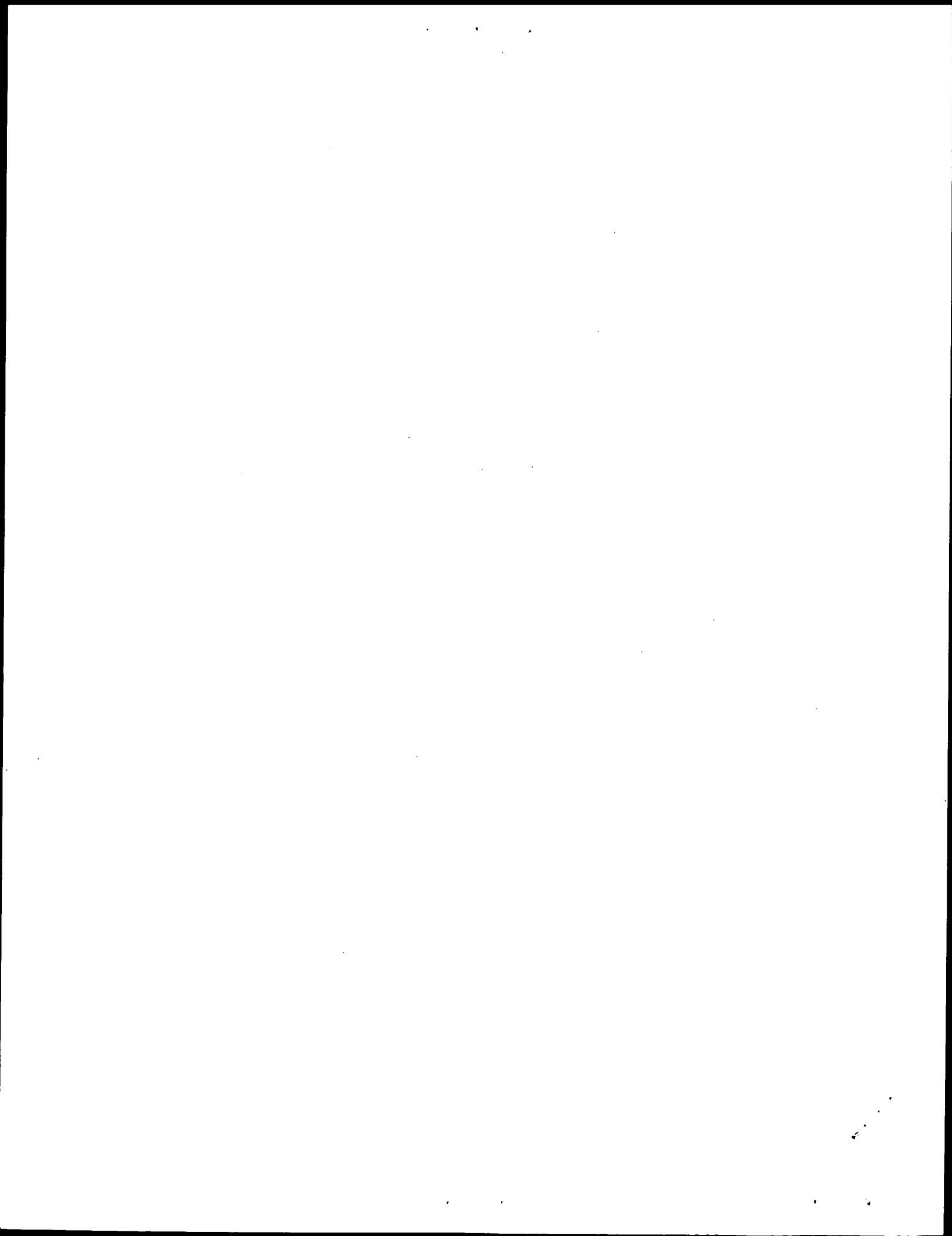
Db 91 EYKNRTYDIANNYSFELLGLLSDRTYTCVQRGESESVVKHITTVESVRADEPTP 150

Qy 120 SISDFEPLTSNRRITCSTSGGFPPEHLSWLENGEELNAINTVSQDPETELYAYSSKLD 179

Db 151 NITESGMPSPADIKRITCFASGGFPKPKLWSLNGREELNTTISODPESELYTISQLD 210

Qy 180 FNMTTNNHNSFMCUJKYGLRVNFTNW 205

Db 211 FNTTYDHFIDCFIEYGAHVSOFNTW 236





FT	Misc-difference	/label= see above			DT	08-APR-1998	(first entry)
FT	Misc-difference	211..213			XX		
FT	Misc-difference	/label= see above			DE	B7-1.	
FT	Misc-difference	226..228			XX		
FT	Misc-difference	/label= see above			KW	Screening; inhibitor; enhancer; binding; CD28; B7-1.	
FT	Misc-difference	232..234			XX		
FT	Domain	/label= see above			OS	Homo sapiens.	
FT	Domain	35..138			XX		
FT	Domain	/label= Ig V-set domain			PN	EP795554-A2.	
FT	Domain	139..236			XX		
XX	W09503408-A.	/label= Ig C-set domain			PD	17-SEP-1997.	
XX	PD	02-FEB-1995.			XX	04-MAR-1997;	97EP-0301438.
XX	PF	26-JUL-1994;	94WO-US08423.		PR	02-OCT-1996;	96JP-0362085.
XX	PR	26-JUL-1993;	93US-0101624.		PR	05-MAR-1996;	96JP-0047795.
PR	19-AUG-1993;	93US-010933.			XX		
PR	03-NOV-1993;	93US-014773.			PA	(TAKE ) TAKEDA CHEM IND LTD.	
XX	PA	(DAND ) DANA FARBER CANCER INST INC.			PI	Hattori M, Hida T, Kurokawa T, Nakanishi A;	
XX	PA	(REPK ) REPLIGEN CORP.			XX		
XX	Freeman GJ, Gray GS, Greenfield E, Nadler LM;				DR	WPI; 1997-450803/42.	
DR	WPI; 1995-075236/10.				DR	N-PSDB; AAW96358.	
XX	N-PSDB; AAO81370.				PS		
PT	Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful				XX	New xanthene derivatives useful as immunomodulators - e.g. methyl	
PT	for enhancing or suppressing T-cell mediated immune responses				PT	2-(carboxymethyl)sulphiny1)-5,7-dichloro-3,8-dihydroxy-6-	
PT	Disclosure; pages 111-113, 175pp; English.				PT	methyl-1-9-oxo-9H-xanthene-1-carboxylate.	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				XX		
CC	cell line Raji, clone no. 13. Its position in the genome is				PS	Fig 4; 117pp; English.	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				XX	The present sequence was used in the development of a novel method	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				CC	to inhibit or enhance binding of CD28	
CC	found in Genbank at Accession No. M27533. The encoded protein,				CC	to B7-1.	
CC	R67989, binds both human CTLA4 and human CD8. It is related				XX	Sequence 288 AA;	
XX	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				SQ		
PS	Sequence 288 AA;				Query	100.0%; Score 1149; DB 16; Length 288;	
XX	CC	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,			Match	100.0%; Score 1149; DB 18; Length 288;	
CC	cell line Raji, clone no. 13. Its position in the genome is				Best Local Similarity	100.0%; Pred. No. 2e-103;	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Matches	0; Mismatches 0; Indels 0; Gaps 0;	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	1 GLSHFCSGVTHVKREVKEYTSLCGHNSVVELAQTRIYQKEKKMVLTMMSGDMNTIWE 60	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	27 g1shfcsgvihvtkeyvatlsrgnvsveelaqtriyqkekkmvltnmsgdmntiwe 60	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	61 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 120	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	121 ISDFEIPITSNIRRITICSTSGGFPEPHLSWLENGEELNAINTVSDPETYAVSSKLDF 180	
XX	Sequence 288 AA;				QY	122 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				Db	123 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	cell line Raji, clone no. 13. Its position in the genome is				QY	124 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Db	125 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	126 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	127 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	128 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	129 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Sequence 288 AA;				QY	130 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				Db	131 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	cell line Raji, clone no. 13. Its position in the genome is				QY	132 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Db	133 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	134 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	135 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	136 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	137 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Sequence 288 AA;				QY	138 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				Db	139 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	cell line Raji, clone no. 13. Its position in the genome is				QY	140 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Db	141 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	142 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	143 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	144 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	145 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Sequence 288 AA;				QY	146 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				Db	147 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	cell line Raji, clone no. 13. Its position in the genome is				QY	148 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Db	149 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	150 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	151 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	152 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	153 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Sequence 288 AA;				QY	154 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				Db	155 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	cell line Raji, clone no. 13. Its position in the genome is				QY	156 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Db	157 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	158 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	159 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	160 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	161 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Sequence 288 AA;				QY	162 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				Db	163 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	cell line Raji, clone no. 13. Its position in the genome is				QY	164 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Db	165 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	166 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	167 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	168 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	169 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Sequence 288 AA;				QY	170 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				Db	171 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	cell line Raji, clone no. 13. Its position in the genome is				QY	172 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Db	173 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	174 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	175 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	176 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	177 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Sequence 288 AA;				QY	178 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				Db	179 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	cell line Raji, clone no. 13. Its position in the genome is				QY	180 YKNRTIFDITNNLSTIVLALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPNPS 146	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Db	181 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	182 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	183 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	184 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	185 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
XX	Sequence 288 AA;				QY	186 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				Db	187 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	cell line Raji, clone no. 13. Its position in the genome is				QY	188 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Db	189 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	190 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	191 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	192 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	193 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
XX	Sequence 288 AA;				QY	194 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
XX	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,				Db	195 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	cell line Raji, clone no. 13. Its position in the genome is				QY	196 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,				Db	197 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be				QY	198 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	found in Genbank at Accession No. M27533. The encoded protein,				Db	199 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	R67989, binds both human CTLA4 and human CD8. It is related				QY	200 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
CC	to human hb7-2 (see Q81351) and murine hb7 (see Q81372).				Db	201 YMTTNHSFMCILKYGHLYRNQTFNWNTKQEHFPDN 216	
XX	Sequence 288 AA;				QY	202 YMTTNHSFMCIL	

PH	Key Peptide	Location/Qualifiers 1..34 /note= "signal peptide"	QY	1 GLSHFCSGVIVHTKEYKEVATLSGGHNVSVELAQTTRIYQKEKRAVLTMMSGDMNTIWPE 60
FT	Protein	35..288 /note= "mature B7 protein"	Db	27 g1shfcsgvivhtkeyevatlsgghnvsveelaqttriyqkekkmltmmgdmntiwpe 86
FT	Domain	35..242 /note= "extracellular domain"	QY	61 YKNRTTIEDTINNLNSIVYLALRPSDEGTYECVVLKYEKDAFKREHLAETVLSSYKADFPPTPS 120
FT	Domain	243..269 /note= "transmembrane domain"	Db	87 yknrttiedtinnlnsivylalrpsdegtycvvlyekdakfrhlaetvlssykaclfptps 146
FT	Domain	270..288 /note= "intracellular domain"	QY	121 ISDFEIPTSNIRRICTSGSGGPEPHSWLNGEEELMAINTVYSQDPETELYAVSSKLDF 180
FT	Modified-site	53..55 /note= "Asn is N-glycosylated"	Db	147 isdfelipstnirriictsgspphephswlengeeelmaintvysqdpeleyavsskldf 206
FT	Modified-site	89..91 /note= "Asn is N-glycosylated"	QY	181 NMTTNHSEFMCMLKYGHHLRVNNQFFNWNTKQEHPDN 216
FT	Modified-site	98..100 /note= "Asn is N-glycosylated"	Db	207 nmtnhsfmclkyghrvngtfnwntkqhnfpdn 242
FT	Modified-site	186..188 /note= "Asn is N-glycosylated"	RESULT 4	
FT	Modified-site	207..209 /note= "Asn is N-glycosylated"	ID AAW73640 standard; Protein; 288 AA.	
FT	Modified-site	211..213 /note= "Asn is N-glycosylated"	XX	
FT	Modified-site	226..228 /note= "Asn is N-glycosylated"	AC AAW73640;	
FT	Modified-site	236..234 /note= "Asn is N-glycosylated"	XX	
FT	Domain	35..139 /note= "Ig V-set domain"	DT 23-MAR-1999 (first entry)	
FT	Domain	140..236 /note= "Ig C-set domain"	XX	
FT	XX	US58598776-A.	DE Human B7-2 antigen.	
PN	XX	PN	XX	
PD	XX	PD	XX	
PD	12-JAN-1999.	PD	19-JAN-1999.	
PF	XX	PF	XX	
PF	03-NOV-1993;	PF	30-MAY-1995;	95US-0456104.
PR	XX	PR	XX	
PR	03-NOV-1993;	PR	30-MAY-1995;	95US-0456104.
XX	(DAND ) DANA FARBER CANCER INST INC.	PR	03-NOV-1993;	93US-0147773.
PA	(HARD ) HARVARD COLLEGE.	XX	XX	
PA	(REPK ) REPLIGEN CORP.	PA	(DAND ) DANA FARBER CANCER INST INC.	
PA	XX	PI	PA	
PI	Baskar S, Freeman GJ, Glimcher LH, Nadler LM, Ostrand-Rosenberg S;	PI	Freeman GJ, Gray GS, Nadler LM;	
XX	WPI: 1999-1130394/11.	XX	XX	
DR	XX	DR	DR	
DR	WPI: 1999-119893/10.	DR	N-PSDB; AAV55786.	
DR	N-PSDB; AAX00757.	XX		
XX	New modified tumour cells - transfected in order to express a T cell costimulatory molecule which allows the induction of an anti-tumour PT response by T cells	PT	Tumour cell transfected to express B7-2 molecule - useful for tumour therapy by stimulating T-cell response	
PT	PT	XX	XX	
PT	New modified tumour cells - transfected in order to express a T cell costimulatory molecule which allows the induction of an anti-tumour PT response by T cells	PS Disclosure; Column 31-34; 24pp; English.	PS Disclosure; Column 37-40; 27pp; English.	
PS	XX	CC	CC	
PS	This sequence represents the amino acid sequence of a human B7 protein. The coding sequence can be used to transfect mammalian tumour (sarcoma) cell so that the B7 protein is expressed by the tumour cell and has the ability to co-stimulate T cells and bind CD28 or CTLA4 ligand.	CC	CC	
PS	The modified tumour cells can be used for inducing an anti-tumour T-lymphocyte response in a subject and are effective against both modified and unmodified tumour cells. The modified tumour cells can also be administered to prevent or inhibit metastatic spread of a tumour or to prevent or inhibit recurrence of a tumour following therapeutic treatment.	CC	CC	
XX	CC	CC	CC	
SQ Sequence	288 AA;	CC	CC	
SQ Sequence	288 AA;	CC	CC	
Query Match	100 %	Score 1149; DB 20; Length 288;	Score 1149; DB 20; Length 288;	
Best Local Similarity	100 %	Pred. No. 2e-103;	Best Local Similarity 100.0%; Fred. No. 2e-103;	
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 GLSHFCSGVIVHTKEYKEVATLSGGHNVSVELAQTTRIYQKEKRAVLTMMSGDMNTIWPE 60	Db	27 g1shfcsgvivhtkeyevatlsgghnvsveelaqttriyqkekkmltmmgdmntiwpe 86	
QY	61 YKNRTTIEDTINNLNSIVYLALRPSDEGTYECVVLKYEKDAFKREHLAETVLSSYKADFPPTPS 120	Qy		

Db 87 yknrtfditnnsiviallpsdegtyecvkyekadfrhealaevtisvkadptps 146  
 CC (macrophage). The fusion proteins or peptides are useful for enhancing or  
 CC suppressing T cell-mediated immune responses, e.g. in situations of  
 CC tissue, skin or organ transplantation, or in graft-versus-host disease.  
 CC The proteins are also useful for enhancing the efficacy of vaccination  
 CC against a variety of pathogens, and may also be used to upregulate an  
 CC immune response against a particular pathogen during an infection or  
 CC against a tumour in a tumour-bearing host.  
 XX

Db 207 rmtnhsfmclikyghlrvnqtnwnttkqshfpdn 242

RESULT 5  
 RAB37087 100.0%; Score 1149; DB 21; Length 288;  
 ID AAB37087 standard; Protein; 288 AA.

XX AAB37087;

XX 28-MAR-2001 (first entry)

XX Human B lymphocyte antigen B7-1.

DE Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;  
 KW antigen; extracellular domain; CTM4; immunoglobulin constant region;

KW immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;  
 KW T cell-mediated immune response; transplantation; vaccination.

XX HOMO sapiens.

XX US6130316-A.

XX 03-NOV-1993.

XX 10-OCT-2000.

XX PA 26-JUL-1994; 94US-0280757.

XX 26-JUL-1993; 93US-0101624.

PR 19-AUG-1993; 93US-0109393.

PR 03-NOV-1993; 93US-0147773.

XX (DAND ) DANA FARBER CANCER INST INC.

PA (REPK ) REPLICIN CORP.

XX Freeman GJ, Nadler LM, Gray GS, Greenfield E;

XX WPI; 2000-655681/63.

DR N-PDB; AAC84051.

XX Disclosure; Column 87-90; 83pp; English.

CC The invention relates to an isolated nucleic acid molecule encoding a first  
 CC fusion protein comprising a first nucleotide sequence encoding a first peptide,  
 CC peptide, and a second nucleotide sequence encoding a second peptide.

CC The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium  
 CC citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C  
 CC to a portion of a nucleotide sequence which encodes a human or murine  
 CC B lymphocyte antigen (B7-2) extracellular domain. The first peptide has  
 CC the ability to bind CD28 or CTLA4; the first peptide has an amino acid  
 CC sequence that is identical or at least 50% identical with the  
 CC extracellular domain of a human B7-2 peptide (AB37085). The second  
 CC peptide is especially an immunoglobulin constant region. This sequence  
 CC represents the human B lymphocyte antigen B7-1. The sequence is used for  
 CC comparison with the B7-2 sequence. The human B7-2 protein is an example  
 CC of a first peptide sequence of the invention. The nucleic acid molecules  
 CC are useful in various expression vectors to direct synthesis of the  
 CC corresponding proteins or peptides in a variety of hosts, particularly  
 CC eukaryotic cells, e.g., mammalian or insect cell culture. The nucleic  
 CC acids are also useful for enhancing the immunogenicity of a mammalian  
 CC cell, e.g., tumour cell (sarcoma) or an antigen presenting cell

Query	Match	Score 100.0%	Length 288;
Best	Local Similarity	100.0%	Pred. No. 2e-103;
Matches	Conservative	0;	Mismatches 0;
			Indels 0;
			Gaps 0;

Qy 1 GLSHFCSGVHVTKEYREVATLSCGHNNSYELAQTRIYKOEKEKRMVLTMMSGDMNTIWIPE 60  
 Db 27 glshfcsgvhvtkeyrevatlscghnnsyelaqtriykoekekrmvltmmsgdmntiwiwe 86

Qy 61 YKNRNTIDITDNNSIVILARPSDEGYTECVLKYEKDAFKREHLIAEVTLSVKADEFPTPS 120  
 Db 87 yknrntiditdnnsivialarpsdegytecvlkyekefkrehaevtlsvkadtpst 146

Qy 121 ISDFEIPTSNIRRIICSTSGGRPEPHLSWLENGEELNAINTVSDPDETELYAVSSKLDF 180  
 Db 147 isdfeiptsnirriicstsfgpephlswlengeelnaintvsdpetelyavsskldf 206

Qy 181 NMTTNHSEMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216  
 Db 207 nmtrnhsemclikyghlrvnqtfnwnttkqehfpdn 242

RESULT 6  
 AAY99966 standard; Protein; 288 AA.  
 ID AAY99966  
 XX  
 AC AAY99966;  
 XX  
 DT 10-JAN-2001 (first entry)  
 XX Human B7 protein.  
 XX  
 B7; human; B cell activation antigen; B lymphocytes;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;  
 KW herpes simplex; influenza; common cold; HIV.  
 XX Homo sapiens.  
 XX  
 DE Human B7 protein.  
 XX  
 FH Key Peptide  
 FT 1..34  
 /label= signal\_peptide  
 FT Domain  
 FT 35..242  
 /label= Extracellular\_domain  
 FT Domain  
 FT 35..138  
 /label= "Ig V-set domain"  
 FT Modified-site  
 FT 53..55  
 /note= "N-linked glycosylation site"  
 FT Modified-site  
 FT 89..91  
 /note= "N-linked glycosylation site"  
 FT Modified-site  
 FT 98..100  
 /note= "N-linked glycosylation site"  
 FT Domain  
 FT 139..236  
 /label= "Ig C-set domain"  
 FT Modified-site  
 FT 186..188  
 /note= "N-linked glycosylation site"  
 FT Modified-site  
 FT 207..209  
 /note= "N-linked glycosylation site"  
 FT Modified-site  
 FT 211..213  
 /note= "N-linked glycosylation site"  
 FT Modified-site  
 FT 226..228  
 /note= "N-linked glycosylation site"  
 FT Modified-site  
 FT 232..234  
 /note= "N-linked glycosylation site"



ID	AAY54920 standard; Protein; 288 AA.	Qy	121 ISDFEIPTSNIRRIGSTSGGFPEPHLSWLENGEELNAINTVSDPTELYAVSSKLDF 180
XX	AAY54920;	Db	147 isdfepptsnirriicstsggfpephlswlengeelnaaintvsdpetylavyasskldf 206
AC			
XX	14-FEB-2000 (first entry)		
DT			
XX	Human B7.1 protein sequence.	Qy	181 NMTTNHSFMCILKYGHURVNOTEWNNTIKQHEFPDN 216
DE		Db	207 nmtnhsfmcikyghurvngtfnwntkjehpdn 242
XX			
RW	Interleukin-12; IL-12; fusion protein; tumour; leukaemia; B7.1 protein.	RESULT 9	
XX		AAU05121	
CS	Homo sapiens.	ID	AAU05121 standard; Protein; 288 AA.
XX	US5994104-A.	XX	
PN		AC	AAU05121;
XX		XX	
PD	30-NOV-1999.	DT	24-OCT-2001 (first entry)
XX		XX	
PF	08-NOV-1996; 96US-0751767.	DE	Colorectal tumour antigen CD80.
XX		XX	
PR	08-NOV-1996; 96US-0751767.	KW	Colorectal cancer; immunostimulant; cytosstatic; immune response;
XX		KW	adenocarcinoma; allotypic tumour cell; SW620 cell; COLO 205 cell;
PA	(UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.	KW	SW403 cell; colon; breast; lung; prostate; cancer; vaccine;
XX		KW	tumour antigen CD80.
PI	Anderson RJ, Prentice HG, MacDonald ID;	XX	
XX		OS	Homo sapiens.
DR	WPI; 2000-038261/03.	XX	
DR	N-PSDB; AAZA40022.	PN	WO200154716-A2.
XX		XX	
PT	Nucleic acid constructs encoding interleukin-12 fusion proteins useful	PD	02-AUG-2001.
XX	for treating leukemia and other cancers -	XX	
PS	Example; Fig 10; 73pp; English.	PF	26-JAN-2001; 2001WO-US02731.
XX		XX	
CC	This sequence represents the human B7.1 protein sequence.	PR	27-JAN-2000; 2000US-0178498.
CC	The invention relates to an isolated nucleic acid construct (I)	XX	PR 28-FEB-2000; 2000US-0183335.
CC	comprising a region encoding an interleukin-12 (IL-12) fusion protein	XX	XX
CC	(comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker	PA	(KINM-) KIMMEL CANCER CENT SIDNEY.
CC	peptide (joining the subunits)) and a region encoding a B7 protein. (I)	XX	PA (IMMU-) IMMUNE RESPONSE CORP.
CC	may be used to produce IL-12 fusion proteins according to standard	XX	
CC	recombinant DNA methodologies. The fusion proteins may be produced either	PI	Sobol RE, Shawler DL, Bartholomew RM, Carlo DJ, Gold DP;
CC	in vitro in a fermentation culture or in vivo as part of a gene therapy	XX	WPI; 2001-502616/55.
CC	protocol (in this case (I) is used to transform a patients cells, which	DR	DR N-PSDB; AAS1426.
CC	then secrete the functional polypeptide to supplement the patients own	XX	
CC	production of IL-12 or to rectify mutations which lead to the expression	XX	
CC	of inactive polypeptides). The fusion proteins produced in this way may	PT	New composition comprising an allogeneic tumour cell, useful for
CC	be used to treat any disease which responds to IL-12 such as tumours	PT	stimulating an immune response in a patient having an adenocarcinoma,
CC	(both solid and dispersed of the kidney, breast, colon, ovarian and	PT	especially useful for treating colorectal, breast, lung or prostate
CC	cervical tumours and melanomas) and in particular, tumours of the blood	XX	cancer -
CC	such as leukemia. Alternatively, the polypeptides may be used as	XX	XX
CC	antigens in the production of antibodies to IL-12 and to assay for	PS	Example 2; Page 130-131; 131pp; English.
CC	CC	XX	
CC	CC	CC	The invention relates to a composition for stimulating an immune response
CC	CC	CC	CC in a patient having an adenocarcinoma or colorectal cancer. The
CC	CC	CC	CC composition comprises an allogeneic tumour cell selected from SW620 cell,
CC	CC	CC	CC COLO 205 cell and SW403 cell, and a physiological carrier. The allogeneic
CC	CC	CC	CC cell stimulates an immune response to an autologous tumour cell in the
CC	CC	CC	CC patient. The composition is useful for stimulating an immune response in
CC	CC	CC	CC a patient having an adenocarcinoma, e.g. colon, breast, lung or prostate
CC	CC	CC	CC adenocarcinoma. The use of allogeneic tumour cells provides a generic
CC	CC	CC	CC source of antigen that can be administered to a variety of patients, in
CC	CC	CC	CC contrast to using autologous tumour cells, which must be isolated from
CC	CC	CC	CC each individual patient. The allogeneic cells are suitable as a cancer
CC	CC	CC	CC vaccine and can stimulate an immune response against autologous tumour
CC	CC	CC	CC cells of a cancer patient. The present sequence represents the amino acid
CC	CC	CC	CC sequence in the method of the invention.
XX	Sequence 288 AA;	XX	
XX		SQ	
Query Match	100.0%; Score 1149; DB 21; Length 288;		
Best Local Similarity	100.0%; Pred. No. 2e-103;		
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 GLSHFCGSVIVHTKEYEVALSGLVQHNVSEELAQPRIWOKRKNVLTMMSGDMNIWIPE 60		
Db	27 gishfcgsvivhtkeyeavalsglvqhvokrknvltmmsgdmniwipe 86		
Qy	61 YKNRTIFDITNNLSIVIALRSDEGTIVCYVLYKEKDAFKREHLAEVTLSVKADFPPTS 120		
Db	87 yknrtifdnnlsivialrsdegtivcyvlykekdafkrehaevtskvadfppts 146		
Query Match	100.0%; Score 1149; DB 22; Length 288;		
Best Local Similarity	100.0%; Pred. No. 2e-103;		
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

QY 1 GLSHFCSGVHTKEYEVALTSCGHNVSVBLLAQTRIYQREKKNVLTMMGDMNTIWPE 60  
 Db 27 gishfcgvhtkeyeavatscghnvsvbllaqtriyqrekknvltmmgdmntiwe 86  
 QY 61 YKNRTIDITNNLISIVTIALRPSDEGYECVYLYKYEKDAFKREHIAEVTLISVKADEFPTPS 120  
 Db 87 yknrtiditnnlisivtialrpsdegyecvylkyekdafkreheiaevtlisvkaadptps 146  
 QY 121 ISDFEIPTSNIIRICSTSGGEPEHLWLGEEELNAINNTVSQDTELYAVSSKLDF 180  
 Db 147 isdfeiptsniiricstsggepehlwlengeeainntvsqdpetelyavssklf 206  
 QY 181 NMTTINHSEPMCLIKYGHYRVNQFENWNNTIQEHPDN 216  
 Db 207 nmtnhsfmclikyghrvnqfnwttkqnfpdn 242

RESULT 10  
 ID AAB19959 standard; Protein; 288 AA.  
 AC AAB19959;  
 XX DT 19-MAR-2001 (first entry)  
 XX DE Human B lymphocyte antigen B7.  
 KW Human; B7; B lymphocyte; antigen; T cell costimulatory molecule;  
 KW CD28; CTIA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;  
 KW metastasis; antitumour; therapy.  
 OS Homo sapiens.  
 FH Key Peptide  
 FT /label= Signal\_peptide  
 Protein  
 FT /label= Mature\_protein  
 Domain  
 FT /note= "extracellular domain"  
 Domain  
 FT /note= "transmembrane domain"  
 Domain  
 FT /note= "intracellular domain"  
 Domain  
 FT /note= "immunoglobulin V-set domain"  
 Domain  
 FT /note= "immunoglobulin C-set domain"  
 FT Modified-site  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site  
 FT /note= "Asn is N-glycosylated"

PA (GEMY ) GENETICS INST INC.  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Baskar S, Glimcher LH, Freeman GJ, Oststrand - Rosenberg S;  
 PI Nadler LM;  
 XX  
 DR WPI; 2001-079388/09.  
 DR DR-N-PSDB; AAA89224.  
 XX  
 PT Modifying tumor cell for treating tumors, reducing metastatic spread,  
 PT inhibiting recurrence of tumor and increasing immunogenicity, involves  
 PT transfecting tumor cells with a nucleic acid encoding B7 molecule  
 XX  
 PS Claim 4: Column 31-34: 24pp; English.  
 XX  
 CC The present sequence is that of human lymphocyte antigen B7, a T  
 CC cell costimulatory molecule that binds to CD28 and CTIA4. Tumour  
 CC cells modified to express a T cell costimulatory molecule,  
 CC especially B7, are disclosed. The tumour cells are modified by  
 CC transfection with a nucleic acid encoding the T cell costimulatory  
 CC molecule, by using an agent which induces or increases expression  
 CC of the T cell costimulatory molecule on the tumour cell surface, or  
 CC by coupling the T cell costimulatory molecule to the tumour cell  
 CC surface. Tumour cells further modified to express major  
 CC histocompatibility complex (MHC) class I and/or class II molecules,  
 CC or in which expression of an MHC associated protein, the invariant  
 CC chain, is inhibited are also disclosed. The modified tumour cells  
 CC are used to treat a patient with a tumour, preventing or inhibiting  
 CC metastatic spread or tumour recurrence. The tumour may be a  
 CC melanoma, a neuroblastoma, a leukaemia or a carcinoma.  
 CC A method for  
 CC specifically inducing a CD4+ T cell response against a tumour, and a  
 CC method for treating a tumour by modification of tumour cells in vivo  
 CC are also disclosed. The treatment methods increase the immunogenicity  
 CC of the tumour cell in vivo. The antitumour T cell-mediated immune  
 CC response is effective both against the modified tumour cells and the  
 CC unmodified tumour cells from which the modified cells were derived.  
 CC Thus, the effector phase of the antitumour response induced by the  
 CC modified tumour cells is not dependent upon expression of a  
 XX  
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 22; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 2e-103; Mismatches 0; Indels 0; Gaps 0;  
 Matches 216; Conservative 0;

QY 1 GLSHFCSGVHTKEYEVALTSCGHNVSVBLLAQTRIYQREKKNVLTMMGDMNTIWPE 60  
 Db 27 gishfcgvhtkeyeavatscghnvsvbllaqtriyqrekknvltmmgdmntiwe 86  
 QY 61 YKNRTIDITNNLISIVTIALRPSDEGYECVYLYKYEKDAFKREHIAEVTLISVKADEFPTPS 120  
 Db 87 yknrtiditnnlisivtialrpsdegyecvylkyekdafkreheiaevtlisvkaadptps 146  
 QY 121 ISDFEIPTSNIIRICSTSGGEPEHLWLGEEELNAINNTVSQDTELYAVSSKLDF 180  
 Db 147 isdfeiptsniiricstsggepehlwlengeeainntvsqdpetelyavssklf 206  
 QY 181 NMTTINHSEPMCLIKYGHYRVNQFENWNNTIQEHPDN 216  
 Db 207 nmtnhsfmclikyghrvnqfnwttkqnfpdn 242

RESULT 11  
 XX AAW41415  
 ID AAW41415 standard; Protein; 473 AA.  
 XX  
 AC AAW41415;  
 XX DT 02-JUN-1998 (first entry)

DE	Human B7.1-murine ASB7 F(ab')2 fusion protein.	KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX	Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region.	KW CD6; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmune disease; allergy; therapy; human; hb7.1glu-glu.
KW		KW XX
XX	Chimeric - Homo sapiens.	OS Chimeric - Homo sapiens.
OS		OS XX
OS	Chimeric - Mus sp.	Chimeric - synthetic.
XX		XX
PN	WO9742329-A1.	Key PH Location/Qualifiers
XX	PD 13-NOV-1997.	Peptide FT 1..34 /note= "potential eukaryotic secretory signal"
XX	PF 29-APR-1997; 97WO-GB01165.	Peptide FT peptide'
XX	PR 14-FEB-1997; 97GB-0003103.	Domain FT 35..242 /note= "human B7.1 (mature protein) extracellular domain"
PR	04-MAY-1996; 96GB-0009405.	FT 243..251 /note= "Glu-Glu detection/purification tag"
PA	(ZENE ) ZENeca LTD.	XX PN WO98589865-A2.
XX		XX PD 30-DEC-1998.
DR	WPI; 1997-558987/51.	XX PF 22-JUN-1998; 98WO-EP03791.
DR	N-P5DB; AAV17340.	XX PR 20-JUN-1997; 97EP-0870092.
XX		XX PA (INNO-) INNOGENETICS NV.
PT	Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis and therapy of cancer	XX PI Bosman A, Buyse M, Lorre K, Sablon E;
PT		XX DR WPI; 1999-105615/09.
XX		XX PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat immune diseases including allograft rejection
PS	Reference Example 3; Page 190-193; 208pp; English.	XX PS Example 3.1.2; Fig 4; 182PP; English.
XX	This sequence is the human B7.1-murine ASB7 F(ab')2 fusion protein (AB7), and is an example of the antibody of the invention. The antibody is an anti-CEA (carcinoembryonic antigen) antibody (preferably 806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be used for in vivo or in vitro diagnosis of cancer.	XX This 29 kDa soluble fusion protein, termed hb7.1glu-glu, is composed of human co-stimulatory molecule B7.1 extracellular domain fused C-terminally to a synthetic Glu-Glu epitope (see AAW90197). It was produced from total RNA of Epstein-Barr virus-transformed human spleen cells by RT-PCR using primers MR67 and MR45 (see AAU01601). The fusion protein has been produced in SF9 Spodoptera frugiperda insect cells using a baculovirus expression system. The invention relates to molecules such as diabodies, trivalent and tetravalent antibodies and small antigen binding peptides which can cross-link, or cross-react with, B7.1 and B7.2 expressed on professional antigen presenting cells leading to the inhibition of antigen-specific T cell activation. Methods to produce such molecules are provided. The molecules are used to treat or prevent diseases of the immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed).
CC		CC Sequence 251 AA;
CC		CC Query Match 99.7%; Score 1146; DB 20; Length 251;
CC		CC Best Local Similarity 99.5%; pred. No. 3.2e-103; Indels 0; Gaps 0;
CC	Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC Matches 215; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	1 GLSHFCSGVTHTEKVEATLSGGHNSVEELAQTRIYQKENKMLVLTMSGDMNIWPE 60	QY 1 GLSHFCSGVTHTEKVEATLSGGHNSVEELAQTRIYQKENKMLVLTMSGDMNIWPE 60
Db	27 gishfcsgvthtekveatlsgghnsveelaqtriywqekkmv1tmmggdmniwpe 86	Db 27 gishfcsgvthtekveatlsgghnsveelaqtriywqekkmv1tmmggdmniwpe 86
QY	61 YKNRTFIDTNISIVILALRPSDEGTVECVLKYKEADFKREHLAEVTLSYKADEFPTPS 120	QY 61 YKNRTFIDTNISIVILALRPSDEGTVECVLKYKEADFKREHLAEVTLSYKADEFPTPS 120
Db	87 yknrtfidoitnnsivialrpsdegtyecvlkykeadfkrehlaeaevtlsvkdftps 146	Db 87 yknrtfidoitnnsivialrpsdegtyecvlkykeadfkrehlaeaevtlsvkdftps 146
QY	121 ISDFEPIPTSNNRRLICSPSGFPSPHLSWLENGEELNANTVSDPTELYAVSSKLD 180	QY 121 ISDFEPIPTSNNRRLICSPSGFPSPHLSWLENGEELNANTVSDPTELYAVSSKLD 180
Db	147 isdfeiptsnrrlicstsggfppehlswlengelnaaintvssqdpetelyavsskldf 206	Db 147 isdfeiptsnrrlicstsggfppehlswlengelnaaintvssqdpetelyavsskldf 206
QY	181 NMNTTNHSFPMCLIXYGHLRVNQNTNWNTTKQEHPDN 216	QY 181 NMTTTNHSFPMCLIXYGHLRVNQNTNWNTTKQEHPDN 216
Db	207 nmtnhsfmclikyghlrvnqtnwnttkqehtpdn 242	Db 207 nmtnhsfmclikyghlrvnqtnwnttkqehtpdn 242
RESULT	12	
ID	AAW90208 standard; Protein: 251 AA.	
XX		
AC	AAW90208;	
XX		
DT	10-MAY-1999 (first entry)	
XX		
DE	hb7.1glu-glu soluble fusion protein.	
XX		

Db	207	rmtnhsfmclikyghlrvngtfnwnttkqghfpdn	242	AC AAW86004; XX	AC AAW86004; XX
	RESULT	13		DT 15-MAR-1999 (first entry)	DT 15-MAR-1999 (first entry)
	AAW38415	AAW38415 standard; Protein; 475 AA.		DE Human B7-1-5T4.1 protein fusion, specific for human 5T4.	DE Human B7-1-5T4.1 protein fusion, specific for human 5T4.
	ID	AAW38415		KW Tumour interacting protein; cancer; gene therapy; vector;	KW Tumour interacting protein; cancer; gene therapy; vector;
	XX			KW 5T4 antigen; monoclonal antibody; single chain antibody;	KW 5T4 antigen; monoclonal antibody; single chain antibody;
	AC	AAW38415;		KW mouse; human; B7-1; co-stimulatory molecule.	KW mouse; human; B7-1; co-stimulatory molecule.
	XX			XX	XX
	DT	08-APR-1998 (first entry)		Chimeric - Mus sp.	Chimeric - Mus sp.
	XX			OS Homo sapiens.	OS Homo sapiens.
	DE	Soluble B7-1-Ig.		OS Chimeric - synthetic.	OS Chimeric - synthetic.
	XX			XX	XX
	KW	Screening; Inhibitor; enhancer; binding; CD28; B7-1;		PN WO9855607-A2.	PN WO9855607-A2.
	KW	soluble B7-1-Ig; immunoglobulin.		XX	XX
	XX			PD 10-DEC-1998.	PD 10-DEC-1998.
	OS	Homo sapiens.		XX	XX
	XX			PF 04-JUN-1998;	PF 04-JUN-1998;
	PN	EP795554-A2.		PR 04-JUL-1997;	PR 04-JUL-1997;
	XX			97GB-0014230.	97GB-0014230.
	PD	17-SEP-1997.		PR 04-JUN-1997;	PR 04-JUN-1997;
	XX			97GB-0011579.	97GB-0011579.
	PF	04-MAR-1997;	97EP-0301438.	PR 20-JUN-1997;	PR 20-JUN-1997;
	XX			97GB-0013150.	97GB-0013150.
	PR	02-OCT-1996;	96JP-02662085.	XX	XX
	PR	05-MAR-1996;	96JP-0047795.	PA (OXFO - OXFORD BIOMEDICA UK LTD.	PA (OXFO - OXFORD BIOMEDICA UK LTD.
	XX			PI Bebbington CR, Carroll MW, Ellard FM, Kingsman SM;	PI Bebbington CR, Carroll MW, Ellard FM, Kingsman SM;
	PA	(TAKE ) TAKEDA CHEM IND LTD.		PI Myers KA;	PI Myers KA;
	XX			XX	XX
	PA	Hattori M, Hida T, Kurokawa T, Nakanishi A;		DR WPI:1999-059910/05.	DR WPI:1999-059910/05.
	XX			N-PSDB; AAV80292.	N-PSDB; AAV80292.
	PT	WPI; 1997-45080342.		XX	XX
	DR	N-PSDB; AAT96359.		PT New vector encoding a tumour interacting protein for treating cancer	PT New vector encoding a tumour interacting protein for treating cancer
	XX			- contains a desired nucleotide sequence and/or protein which	- contains a desired nucleotide sequence and/or protein which
	PT	New xanthene derivatives useful as immunomodulators - e.g. methyl		PT recognises tumours, and is used as a gene delivery system to treat	PT recognises tumours, and is used as a gene delivery system to treat
	PT	2-(carboxymethylsulphonyl)-5,7-dichloro-3,8-dihydroxy-6-		PT cancer	PT cancer
	PT	methyl-9-oxo-9-H-xanthene-1-carboxylate.		XX	XX
	PS	Disclosure; Fig 6 and 7; 117pp; English.		PS Example 5; Fig 2; 82pp; English.	PS Example 5; Fig 2; 82pp; English.
	XX			XX This is the amino acid sequence of B7-1-5T4.1, a fusion protein	XX This is the amino acid sequence of B7-1-5T4.1, a fusion protein
	CC	The present sequence was used in the development of a novel method		CC comprising the extracellular domain (amino acids 1-215) of human	CC comprising the extracellular domain (amino acids 1-215) of human
	CC	for screening for compounds that inhibit or enhance binding of CD28		CC co-stimulatory molecule B7-1 joined via a flexible peptide linker	CC co-stimulatory molecule B7-1 joined via a flexible peptide linker
	CC	to B7-1.		CC to an scFv (see AAV80292) derived from murine 5T4 monoclonal	CC to an scFv (see AAV80292) derived from murine 5T4 monoclonal
	CC	antibody, B7-1-5T4.1 cDNA (see AAV80292) can be inserted into vector		CC antibody, B7-1-5T4.1 cDNA (see AAV80292) can be inserted into vector	CC antibody, B7-1-5T4.1 cDNA (see AAV80292) can be inserted into vector
	CC	PCI to allow expression of the fusion protein in mammalian cells.		CC PCI to allow expression of the fusion protein in mammalian cells.	CC PCI to allow expression of the fusion protein in mammalian cells.
	CC	The trophoblast cell surface antigen defined by 5T4 is expressed at		CC The trophoblast cell surface antigen defined by 5T4 is expressed at	CC The trophoblast cell surface antigen defined by 5T4 is expressed at
	CC	high levels on the cells of a wide variety of human tumours. The		CC high levels on the cells of a wide variety of human tumours. The	CC high levels on the cells of a wide variety of human tumours. The
	CC	invention relates to a vector comprising a nucleotide sequence		CC invention relates to a vector comprising a nucleotide sequence	CC invention relates to a vector comprising a nucleotide sequence
	CC	coding for a tumour interacting protein (TIP) and optionally a		CC coding for a tumour interacting protein (TIP) and optionally a	CC coding for a tumour interacting protein (TIP) and optionally a
	CC	nucleotide sequence of interest (NOI) which encodes a protein of		CC nucleotide sequence of interest (NOI) which encodes a protein of	CC nucleotide sequence of interest (NOI) which encodes a protein of
	CC	interest (POI), the vector being capable of delivering the NOI		CC interest (POI), the vector being capable of delivering the NOI	CC interest (POI), the vector being capable of delivering the NOI
	CC	and/or POI to the tumour recognised by the TIP. Delivery can be in		CC and/or POI to the tumour recognised by the TIP. Delivery can be in	CC and/or POI to the tumour recognised by the TIP. Delivery can be in
	CC	vivo or ex vivo. The vector is used to treat cancer, and may also		CC vivo or ex vivo. The vector is used to treat cancer, and may also	CC vivo or ex vivo. The vector is used to treat cancer, and may also
	CC	used as a gene delivery system for introducing at least 1 gene		CC used as a gene delivery system for introducing at least 1 gene	CC used as a gene delivery system for introducing at least 1 gene
	CC	encoding a TIP (preferably a tumour binding protein) into a		CC encoding a TIP (preferably a tumour binding protein) into a	CC encoding a TIP (preferably a tumour binding protein) into a
	CC	haematopoietic cell lineage. B7-1 is expected to bind specifically		CC haematopoietic cell lineage. B7-1 is expected to bind specifically	CC haematopoietic cell lineage. B7-1 is expected to bind specifically
	CC	to CD28 and CTLA-4 present on human T-cells.		CC to CD28 and CTLA-4 present on human T-cells.	CC to CD28 and CTLA-4 present on human T-cells.
	SQ	Sequence 475 AA;		XX Sequence 488 AA;	XX Sequence 488 AA;
	Query	Match 99.6%; Score 1144; DB 18; Length 475;		Query Match 99.5%; Score 1143; DB 20; Length 488;	Query Match 99.5%; Score 1143; DB 20; Length 488;
	Best	Local Similarity 99.5%; Pred. No. 1.2e-102;		Best Local Similarity 100.0%; Pred. No. 1.6e-102;	Best Local Similarity 100.0%; Pred. No. 1.6e-102;
	Matches	Mismatches 1; Indels 0; Gaps 0;		Mismatches 0; Indels 0; Gaps 0;	Mismatches 0; Indels 0; Gaps 0;
	215;	Conservative		Matches 215; Conservative	Matches 215; Conservative
Qy	1	GLSHFCSGVTHVTKEYKEVATLSCGHNVSYEEAQTTRIYQKEKKMVLTTMSGDMNWIPE	60	Qy 1 GLSHFCSGVTHVTKEYKEVATLSCGHNVSYEEAQTTRIYQKEKKMVLTTMSGDMNWIPE	60
Db	27	9lsfhfcsgvhvtkeykevatlscghnvsyeeaqtriywqkekkmvmtms9dmnwipe	86	Db 27 glsfhfcsgvhvtkeykevatlscghnvsyeeaqtriywqkekkmvmtms9dmnwipe	86
Qy	61	YKNRTFDITNNLSIVILARPSDEGTYECVVRYKEKDAFKREHLAEVTVLSVKADEPPS	120	Qy 61 YKNRTFDITNNLSIVILARPSDEGTYECVVRYKEKDAFKREHLAEVTVLSVKADEPPS	120
Db	87	yknrifdtnlnsivialrpsdegtycvvkyekdafkrehlaevtsvkadfppls	146	Db 87 yknrtifdtnlnsivialrpsdegtycvvkyekdafkrehlaevtsvkadfppls	146
Qy	121	ISDFEIPTSNIRRITCSTSGFPPEPHLSWENGEELNAINNTYSQDPETELYAVSSKLDF	180	Qy 121 ISDFEIPTSNIRRITCSTSGFPPEPHLSWENGEELNAINNTYSQDPETELYAVSSKLDF	180
Db	147	isdfciptnirriicsts9gfpelvsiengneainnttysqdpelvsiayrskldf	206	Db 147 isdfciptnirriicsts9gfpelvsiengneainnttysqdpelvsiayrskldf	206
Qy	181	NMTTNHSFMOLIKYGHLRNQTFNWNTTKQEHFPDN	216	Qy 181 NMTTNHSFMOLIKYGHLRNQTFNWNTTKQEHFPDN	216
Db	207	nmtnhsfmolikyghlrnqtfnwnttkqehfpdh	242	Db 207 nmtnhsfmolikyghlrnqtfnwnttkqehfpdh	242
RESULT	14	AAW86004 standard; Protein; 488 AA.			
ID	AAW86004				
	XX				

Qy 121 ISDFEIPTSNIRRIGCSTSGGFPEPHLSWLENGEELNAINTVSDPTELYAVSSKLDF 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 147 isdfelptsnrricstsggfpephlswlengelnaaintvsdpteleyavsskldf 206  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Qy 181 NMTTNHSFMCILIKYGHLRVNGTFWNNTTKOEHFPD 215  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 207 nmttnhsfmcilikyghlrvngtfwnnttkoehfpd 241  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 RESULT 15  
 AAB83836 ID AAB83836 standard; Protein; 488 AA.  
 XX AC AAB83836;  
 XX DT 23-JUL-2001 (first entry)  
 XX DE Amino acid sequence of a B7-1.5T4.1 fusion protein.  
 XX KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;  
 KW hypersensitivity; autoimmune disease; central nervous system disorder;  
 KW Parkinson's disease; periodontal disease; cardiopulmonary disease;  
 KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;  
 KW Helicobacter-related disease; immune disorder.  
 OS Synthetic.  
 OS Mus sp.  
 OS Homo sapiens.  
 XX PN WO200136486-A2.  
 PD 25-MAY-2001.  
 XX PF 13-NOV-2000; 2000WO-GB04317.  
 XX PR 18-NOV-1999; 99WO-GB03859.  
 PR 15-FEB-2000; 2000GB-0003527.  
 PR 02-MAR-2000; 2000GB-0005071.  
 PA (OXFO ) OXFORD BIOMEDICA UK LTD.  
 XX PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;  
 PI Myers KA,  
 XX DR WPI; 2001-343805/36.  
 DR N-P5DB; AAF89730.  
 XX PT Use of single chain antibody capable of recognizing a disease  
 PT associated molecule for manufacturing a medicament for preventing  
 PT and/or treating a disease condition associated with disease associated  
 PT molecule -  
 XX PS Claim 3; Fig 2; 118pp; English.

CC The specification describes the use of a single chain antibody (ScFv),  
 CC which is capable of recognizing a disease associated molecule in the  
 CC manufacture of a medicament for the prevention and treatment of a  
 CC disease condition. The ScFv antibody is useful in the manufacture of  
 CC a medicament, for affecting a disease in vivo, for preparing a  
 CC pharmaceutical composition for in vivo imaging and/or for adjuvant  
 CC treatment of a disease. The ScFv antibody is also useful for  
 CC treating inflammatory diseases including arthritis, hypersensitivity,  
 CC autoimmune diseases, cancers, central nervous system disorders  
 CC including Parkinson's disease, periodontal diseases, cardiopulmonary  
 CC diseases, cardiovascular diseases, gastrointestinal disorders,  
 CC infections, diabetics, Helicobacter-related diseases, and other immune  
 CC disorders. The present sequence represents a B7-1.5T4.1 fusion protein.  
 CC This comprises the N-terminus of the 5T4 ScFv is fused after amino acid  
 CC 215 of human B7-1.  
 XX Sequence 488 AA;

Query Match 99.5%; Score 1143; DB 22; Length 488;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-102;  
 Matches 215; Conservative 0; Indels 0; Gaps 0;  
 Qy 1 GLSHFCGSVIIHVTKEYEVATLSCGHNVSVEELAQTRIYQKEKAMVLTMMSGDMNIWPE 60  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 27 qishfcgsvhvtkeyevatlscghnvsveelaqtriyqkekamvltmmsgdmniwpe 86  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Qy 61 YKNRTSPFDITNNLSIVLALRPSDETYECVVKYERDAFREHLAETSVKADEFPTPS 120  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 87 yknrtspfditnnlsivlalrpsdegyecvvlkyekdafrrehaetsvkadftps 146  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Qy 121 ISDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSDPTELYAVSSKLDF 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 147 isdfelptsnrricstsggfpephlswlengelnaainttvsqdpetelyavsskldf 206  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Qy 181 NMTTNHSFMCILIKYGHLRVNGTENRNTTKOEHFPD 215  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 207 nmtttfsfmcilikyghlrvngtfnwnttkoehfpd 241  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Search completed: April 24, 2002, 15:30:21  
 Job time: 252 sec







IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic

NAME/KEY: extracellular domain  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: 19 C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: 19 V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: FREEDMAN, ARNOLD S.  
 AUTHORS: SEGAL, JEFFREY M.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
 US-08-147-772-2

Query Match	Score 1149;	DB 2;	Length 288;
Best Local Similarity	100.0%;	Pred. No. 4	7e-113;
Matches	216;	Mismatches	0;
Indels	0;	Gaps	0;

Qy 1 GLSHFCGGVHYTKKEVATLSCGHNVSVEEAQTQYWKKEKKMVLTMMSGDMNIWPE 60  
 Db 27 GLSHFCGGVHYTKKEVATLSCGHNVSVEEAQTQYWKKEKKMVLTMMSGDMNIWPE 86

Qy 61 YKNRNTIFDTNNLSIVTLLRPSDEGTYECVVLYKEFDAFKREHLAEVTLSVKADFPTPS 120  
 Db 87 YKNRNTIFDTNNLSIVTLLRPSDEGTYECVVLYKEFDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPSNIRLICSTSGGFPFPHLSWLENGEELNAINTVSDQPETEPELYAVSSKLDF 180  
 Db 147 ISDFEIPSNIRLICSTSGGFPFPHLSWLENGEELNAINTVSDQPETEPELYAVSSKLDF 206

Qy 181 NMTTNHSPMCLIKYGLRVNQTFNWNTTKQEHFPDN 216  
 Db 207 NMTTNHSPMCLIKYGLRVNQTFNWNTTKQEHFPDN 242

RESULT 2  
 US-08-456-104-6  
 Sequence 6, Application US/08456104  
 Patent No. 5861310  
 GENERAL INFORMATION:  
 APPLICANT: Freeman, Gordon J.  
 ATTORNEY: Nadler, Lee M.  
 APPLICANT: Gray, Gary S.  
 TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 CITY: Boston  
 STATE: Massachusetts  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/456,104  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/101,624;  
 FILING DATE: 26-JUL-1993;  
 APPLICATION NUMBER: 08/109,393;  
 APPLICATION NUMBER: 19-AUG-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: RPI-008  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-456-104-6

---

Query Match      100.0%;    Score 1149;    DB 2;    Length 288;  
 Best Local Similarity 100.0%;    Pid. No. 4.7e-13;    Length 288;  
 Matches 216;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;

Qy	1	GISHFCSGVHIVTKEYKEVATLSCGHNVSVEELAQPRIYKWEKEKAVLTLMSGDMMNIWPE	60
Db	27	GISHFCSGVHIVTKEYKEVATLSCGHNVSVEELAQPRIYKWEKEKAVLTLMSGDMMNIWPE	86
Qy	61	YKNRTIDITNNLSTYLALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADEFPTPS	120
Db	87	YKNRTIDITNNLSTYLALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADEFPTPS	146
Qy	121	ISDFEIPTSNIRRICITSGGPPPEPHLSWLEGEELNAINTVSDQPETELYAVSSKLDF	180
Db	147	ISDFEIPTSNIRRICITSGGPPPEPHLSWLEGEELNAINTVSDQPETELYAVSSKLDF	206
Qy	181	NMTTNHSPMCLKYGHLRVQENWNNTKQHEFPDN	216
Db	207	NMTTNHSPMCLKYGHLRVQENWNNTKQHEFPDN	242

---

RESULT 3  
 US-08-101-624-23  
 Sequence 23, Application US/08101624

GENERAL INFORMATION:  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 APPLICANT: Gray, Gary S.  
 TITLE OF INVENTION: No. 5942607 el CTLA4/CD28 Ligands and  
 TITLE OF INVENTION: Uses Therefor  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHVE & COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 01109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentent Release #1.0, Version #1.125  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/101,624  
 FILING DATE: 26-JUL-1993  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: RPI-004  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: B cell activation antigen; natural ligand  
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein

FEATURE: signal sequence  
 NAME/KEY: -34 to -1  
 LOCATION: amino terminal sequencing of  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic

FEATURE: extracellular domain  
 NAME/KEY: 1 to 208  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: transmembrane domain  
 NAME/KEY: 209 to 235  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: intracellular domain  
 NAME/KEY: 236 to 254  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: N-linked glycosylation  
 NAME/KEY: 19 to 21  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: N-linked glycosylation  
 NAME/KEY: 55 to 57  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: N-linked glycosylation  
 NAME/KEY: 64 to 66  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: N-linked glycosylation  
 NAME/KEY: 152 to 154  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: N-linked glycosylation  
 NAME/KEY: 173 to 175  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: N-linked glycosylation  
 NAME/KEY: 177 to 179  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: N-linked glycosylation  
 NAME/KEY: 192 to 194  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: N-linked glycosylation  
 NAME/KEY: 198 to 200  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: Ig V-set domain  
 NAME/KEY: 1 to 104  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE: Ig C-set domain  
 NAME/KEY: 105 to 202  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.

; AUTHORS: FREEDMAN, ARNOLD S.  
 ; AUTHORS: SEGILLI, JEFFREY M.  
 ; AUTHORS: LEE, GRACE  
 ; AUTHORS: WHITMAN, JAMES F.  
 ; AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262  
 US-08-101-024-23

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; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-751-767A-6

Query Match 100.0%; Score 1149; DB 2; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-113;  
 Matches 216; Conserv 0; Indels 0; Gaps 0;

QY 1 GLSHFCGIVHVTKEYEATLSCGHNSVVELAQTRIYQKEKAVMVLTMMSGDMNIWPE 60  
 Db 27 GLSHFCGIVHVTKEYEATLSCGHNSVVELAQTRIYQKEKAVMVLTMMSGDMNIWPE 86

QY 61 YKNRTIFDTNNLSIVLALRPSDETYECVLYKADEFPTPS 120  
 Db 87 YKNRTIFDTNNLSIVLALRPSDETYECVLYKADEFPTPS 146

QY 121 ISDFEPTSNIRRICSTSGFPFEPHLWSLNGEELNAINTVSQDPETELYAVSSKLDF 180  
 Db 147 ISDFEPTSNIRRICSTSGFPFEPHLWSLNGEELNAINTVSQDPETELYAVSSKLDF 206

QY 181 NMTTNHSFMCMLIKYGLRVNOTFNWNTTKQEHFPDN 216  
 Db 207 NMTTNHSFMCMLIKYGLRVNOTFNWNTTKQEHFPDN 242

RESULT 5  
 US-08-153-262-2  
 ; Sequence 2, Application US/08153262  
 ; Patent No. 6071716

; GENERAL INFORMATION:  
 ; APPLICANT: FREEMAN, GORDON J.  
 ; APPLICANT: FREEDMAN, ARNOLD S.  
 ; APPLICANT: NADLER, LEE M.  
 ; TITLE OF INVENTION: DNA Encoding B7, A New Member  
 ; OF The IgG Superfamily With Unique Expression On  
 ; Activated And Neoplastic B Cells.  
 ; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: The Dana-  
 ; Barber Cancer Institute  
 ; STREET: 44 Binney Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02115  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage  
 ; COMPUTER: IBM Personal System 2; Model 30  
 ; OPERATING SYSTEM: MS/DOS  
 ; SOFTWARE: Wordperfect 5.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/153-262  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/751,306  
 ; FILING DATE: 28-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: HARP, JULIA D.  
 ; REGISTRATION NUMBER: 33132  
 ; REFERENCE/DOCKET NUMBER: DFCI-116.1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (203) 255-8900  
 ; TELEFAX: (203) 259-2846  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 288 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; DESCRIPTION:  
 ; for CD28 T cell surface antigen; natural ligand  
 ; for CD28 T cell surface antigen; transmembrane protein

; RESULT 4  
 US-08-751-767A-6  
 ; Sequence 6, Application US/08751767A  
 ; Patent No. 5994104

; GENERAL INFORMATION:  
 ; APPLICANT: ANDERSON, ROBERT J.  
 ; APPLICANT: GRANT, HUGH  
 ; APPLICANT: MACDONALD, IAN D.  
 ; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN  
 ; NUMBER OF SEQUENCES: 80  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: NIXON & VANDERHYE P.C.  
 ; STREET: 1100 NORTH GLEBE ROAD  
 ; CITY: ARLINGTON  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22201  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/751,767A  
 ; FILING DATE: 08-NOV-1996  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: SADOFF, B.J.  
 ; REGISTRATION NUMBER: 36,663  
 ; REFERENCE/DOCKET NUMBER: 117-221  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 7038164100  
 ; TELEFAX: 7038164100  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: ~ 288 amino acids

FEATURE:  
NAME/KEY: signal sequence  
LOCATION: -34 to -1  
IDENTIFICATION METHOD: amino terminal sequencing of  
IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic

FEATURE:  
NAME/KEY: extracellular domain  
LOCATION: 1 to 208  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 209 to 235  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: intracellular domain  
LOCATION: 236 to 254  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 19 to 21  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 55 to 57  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 64 to 66  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 152 to 154  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 173 to 175  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 177 to 179  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 192 to 194  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: Ig V-set domain  
LOCATION: 1 to 104  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: Ig C-set domain  
LOCATION: 105 to 202  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

AUTHORS: FREEDMAN, ARNOLD S.  
AUTHORS: SEGIL, JEFFREY M.  
AUTHORS: LEE, GRACE F.  
AUTHORS: WHITMAN, JAMES F.  
AUTHORS: NADLER, LEE M.  
TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
US-08-153-262-2

Query Match 100.0%; Score 1149; DB 3; Length 288;  
Best Local Similarity 100.0%; Ped. No. 4 7e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCGVITHKVEVATLSCGHNVSVELAQTTRYWQKEKKMVLTMMSGDMNTWPE 60  
Db 27 GLSHFCGVITHKVEVATLSCGHNVSVELAQTTRYWQKEKKMVLTMMSGDMNTWPE 86

Qy 61 YKRTTIEDTNNSIVILALRPSDEGYECVVKYKEVDAFKREHLAEVTLSYKADFPFPPS 120  
Db 87 YKRTTIEDTNNSIVILALRPSDEGYECVVKYKEVDAFKREHLAEVTLSYKADFPFPPS 146

Qy 121 ISDPEIPTSNRITCSTSGGFPPEPHLSMLENGBELNAINNTVSQDPETELYAVSSKLDF 180  
Db 147 ISDPEIPTSNRITCSTSGGFPPEPHLSMLENGBELNAINNTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGLRVNOTFWNTTKQEHHFDN 216  
Db 207 NMTTNHSFMCLIKYGLRVNOTFWNTTKQEHHFDN 242

RESULT 6  
US-08-479-744A-29  
Sequence 29, Application US/08479744A  
Patent No. 6084067

GENERAL INFORMATION:  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.  
APPLICANT: Gray, Gary S.  
TITLE OF INVENTION: N 6084067e1 CTLA4/CD28 Ligands and  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,744A  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/280,757  
FILING DATE: 26-JUL-1994  
APPLICATION NUMBER: 08/109,393  
FILING DATE: 28-AUG-1993  
APPLICATION NUMBER: 08/101,244  
FILING DATE: 26-JULY-1993  
APPLICATION NUMBER: 08/147,773  
FILING DATE: 3-NOV-1993

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Mandrajous, Amy E.
; REGISTRATION NUMBER: 36,207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEXFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand; transmembrane protein
; for CD28 T cell surface antigen; transmembrane protein

; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of
; OTHER INFORMATION: soluble protein
; FEATURE:
; NAME/KEY: hydrophobic
; LOCATION: 1 to 208
; IDENTIFICATION METHOD: hydropathic
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: extracellular domain
; LOCATION: 209 to 235
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 236 to 254
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 19 to 21
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 55 to 57
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 64 to 66
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 152 to 154
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 173 to 175
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 177 to 179
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 192 to 194
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; NAME/KEY: N-linked glycosylation

; LOCATION: 198 to 200
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig C-set domain
; LOCATION: 105 to 202
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; PUBLICATION INFORMATION:
; AUTHORS: FREEMAN, GORDON J.
; AUTHORS: FREEDMAN, ARNOLD S.
; AUTHORS: SEGIL, JEFFREY M.
; AUTHORS: LEE, GRACE F.
; AUTHORS: WHITMAN, JAMES F.
; AUTHORS: NADLER, LEE M.
; TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells
; JOURNAL: The Journal of Immunology
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
; US-08-479-744A-29

; Query Match Score 1149; DB 3; Length 288;
; Best Local Similarity 100.0%; Pred. No 4, 7e-113;
; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 1 GLSHFCSGVTHVTKEVATLSCGHNTSVEELAQTRLYQEKKKMVLTTMSGDMNIWPE 60
; Db 27 GLSHFCSGVTHVTKEVATLSCGHNTSVEELAQTRLYQEKKKMVLTTMSGDMNIWPE 86

; Qy 61 YKNNTIFDTNNLSIVIALRPSDEGTTECVVLYKEKDAFKREHLAEYTLSVRADEPPTPS 120
; Db 87 YKNNTIFDTNNLSIVIALRPSDEGTBCVWLYKEKDAFKREHLAEYTLSVRADEPPTPS 146

; Qy 121 ISDPEIPTSNIRRLLCSGGFPPEPHLSWLENGLELNAINTVSQDPETELYAVSKLDF 180
; Db 147 ISDPEIPTSNIRRLLCSGGFPPEPHLSWLENGLELNAINTVSQDPETELYAVSKLDF 206

; Qy 181 NMPTTNHSPMCNLKLYGHLRVYNQTFNWNTPKQEHFPDN 216
; Db 207 NMPTTNHSPMCNLKLYGHLRVYNQTFNWNTPKQEHFPDN 242

; RESULT 7
; US-08-280-757B-29
; Sequence 29, Application US/08280757B
; Patent No. 6130116
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: NC-6130316el CTLA4/CD28 Ligands and Uses Therefor
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;
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COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/280,757B  
 FILING DATE: 26-JUL-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/101,624  
 FILING DATE: 26-JULY-1993  
 APPLICATION NUMBER: 08/109,393  
 FILING DATE: 19-AUG-1993  
 APPLICATION NUMBER: 08/147,773  
 FILING DATE: 3-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: RPI-004CP2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: B cell activation antigen; natural ligand  
 for CD28 T cell surface antigen; transmembrane protein  
 FEATURE:  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic  
 FEATURE:  
 NAME/KEY: extracellular domain  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD:  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175

IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: FREEDMAN, ARNOLD S.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With  
 Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262  
 US-08-280-757B-29

Query Match 100.0% Score 1149; DB 4; Length 288;  
 Best Local Similarity 100.0%; Fred. No. 4.7-e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFGSGVHTVKVEVATLSCGGHNVSYELAQTRIYRKEKKMVLTMMSGDMNMWIPE 60  
 Db 27 GLSHFGSGVHTVKVEVATLSCGGHNVSYELAQTRIYRKEKKMVLTMMSGDMNMWIPE 86  
 Qy 61 YKNRTFDITNNLNLTVLARPSDETYECVLYKFDKFREHLAEVTSVKADPPTPS 120  
 Db 87 YKNRTFDITNNLNLTVLARPSDETYECVLYKFDKFREHLAEVTSVKADPPTPS 146  
 Qy 121 ISDFEPTSNIRRIGTSGGFPPEHLNVTWNTTKQEHFPDN 180  
 Db 147 ISDFEPTSNIRRIGTSGGFPPEHLNVTWNTTKQEHFPDN 206  
 Qy 181 NMTTNHSFMCLIKYGHLRVNQTENWNTTKQEHFPDN 216  
 Db 207 NMTTNHSFMCLIKYGHLRVNQTENWNTTKQEHFPDN 242

RESULT 8  
 US-09-159-135-2  
 Sequence 2, Application US/09159135  
 Patent No. 619905  
 GENERAL INFORMATION:  
 APPLICANT: Ostrand-Rosenberg, Suzanne  
 APPLICANT: Baskar, Sivasubramanian

APPLICANT: Glimcher, Laurie H.  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 NUMBER OF INVENTION: Tumor Cells With Increased Immunogenicity  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAITNE & COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/159,135  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/147,772  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Any E.  
 REGISTRATION NUMBER: 36,207  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: B cell activation antigen; natural ligand  
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
 FEATURE:  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic  
 FEATURE:  
 NAME/KEY: extracellular domain  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66

IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEDMAN, ARNOLD S.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of the Ig Superfamily With  
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
 US-09-159-135-2

Query Match 100.0% Score 1149; DB 4; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GLSHFCSGVTHVKVEVKEYLPSDEGTVCVLYERDAFKRELAETVLSVADFPPLS 120  
 Db 27 GLSHFCSGVTHVKVEVATLSGHNVSEELAQTTRYWQEKKMLTMMMSGDMNIWDE 86

QY 61 YKNTIDITNNISIVIALRPSDEGTVCVLYERDAFKRELAETVLSVADFPPLS 120  
 Db 87 YKRTIDITNNISIVIALRPSDEGTVCVLYERDAFKRELAETVLSVADFPPLS 146

QY 121 ISDFEIPSNIRITCSSTGGFPPEPHSLWLENGEELNAINTVYSDPPTELYAVSSKLDF 180  
 Db 147 ISFEIPSNIRITCSSTGGFPPEPHSLWLENGEELNAINTVYSDPPTELYAVSSKLDF 206

QY 181 NMFTTNHSPMCLIKYGHFLRVNOTFNWNTKQEHEFPDN 216

Db	207	NMTTNNHSFMCILKYGHLRVQTFNWNTTKQEHFPDN	242
RESULT	9		
US-08-205-697A-19			
; Sequence 19, Application US/08205697A			
; Patent No. 6218510			
; GENERAL INFORMATION:			
; APPLICANT: Sharpe, Arlene H.			
; ADDRESS: Borrillio, Francescopaolo			
; APPLICANT: Freiman, Gordon J.			
; ADDRESS: LAHIVE & COCKFIELD			
; STREET: 60 State Street, suite 510			
; CITY: Boston			
; STATE: Massachusetts			
; COUNTRY: USA			
; ZIP: 02109-1875			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: ASCII Text			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/205, 697A			
; FILING DATE: 02-Mar-1994			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Mandragouras, Amy E.			
; REGISTRATION NUMBER: 36, 207			
; REFERENCE/DOCKET NUMBER: BWI-120			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (617)227-7100			
; TELEFAX: (617)227-5941			
; INFORMATION FOR SEQ ID NO: 19:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 288 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
; US-08-205-697A-19			
Query Match	100.0%	Score 1149;	DB 4;
Best Local Similarity	100.0%	Pred. No. 4	Length 288;
Matches	216;	Conservative	0;
		Mismatches	0;
		Indels	0;
		Gaps	0;
Qy	1	GLSHFCGSVIVTKVEKATLSCGHNVSYVLELAQTRIYNOKEKKMVLTMMSGDMNIWPE	60
Db	27	GLSHFCGSVIVTKVEKATLSCGHNVSYVLELAQTRIYNOKEKKMVLTMMSGDMNIWPE	86
Qy	61	YKNRTIEDTNNSLIVTLARPSDEGTYYCIVLKYEKDAFKREHLAEVTLSVKADEPTPS	120
Db	87	YKNRTIEDTNNSLIVTLARPSDEGTYYCIVLKYEKDAFKREHLAEVTLSVKADEPTPS	146
Qy	121	ISDFEPTSNRTRICSTGGPEPHISWLVGEELNAINTVSQDPPETLYAVSSKLDF	180
Db	147	ISDFEPTSNRTRICSTGGPEPHISWLVGEELNAINTVSQDPPETLYAVSSKLDF	206
Qy	181	NMTTNNHSFMCILKYGHLRVQTFNWNTTKQEHFPDN	216
Db	207	NMTTNNHSFMCILKYGHLRVQTFNWNTTKQEHFPDN	242
RESULT	10		
US-08-702-575-19			
; Sequence 19, Application US/08702575			
; Patent No. 6294660			
; GENERAL INFORMATION:			
; APPLICANT: Sharpe, Arlene H.			

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; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
; US-09-171-945-131

Query Match          100.0%;  Score 1149;  DB 4;  Length 473;
Best Local Similarity 100.0%;  Pred. No. 1e-112;
Matches 216;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 GLSHFCGSVTHVKVEVKEYATLSCGHNVSYEELAQTRIYQKEKKAVLTMMGDMNIMPE 60
Db      27 GLSHFCGSVTHVKVEVKEYATLSCGHNVSYEELAQTRIYQKEKKAVLTMMGDMNIMPE 86
Qy      61 YKNRTIDITNNLSIVILALRPSDGTYYECVVLKYERDAFKREHLAETVLSYKADFPPIPS 120
Db      87 YKRTIDITNNLSIVILALRPSDGTYYECVVLKYERDAFKREHLAETVLSYKADFPPIPS 146
Qy      121 ISDFEIPTSNIRRICSTSGGFPEPHISWLENGEELNAINTVSDPETYAVSSKLDF 180
Db      147 ISDFEIPTSNIRRICSTSGGFPEPHISWLENGEELNAINTVSDPETYAVSSKLDF 206
Qy      181 NMTTNHSFMCLIKYGHLYRNQTFNWNTTKQEHFPDN 216
Db      207 NMTTNHSFMCLIKYGHLYRNQTFNWNTTKQEHFPDN 242

RESULT 13
US-08-630-172-15
; Sequence 15, Application US/08630172
; Patent No. 606054
; GENERAL INFORMATION:
;   APPLICANT: Staerz, Uwe
;   TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
;   NUMBER OF SEQUENCES: 41
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Sheridan Ross & McIntosh
;     STREET: 1700 Lincoln Street, 35th Floor
;     CITY: Denver
;     STATE: Colorado
;     COUNTRY: U.S.
;     ZIP: 80203
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0., Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/630-172
;   FILING DATE:
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Connell, Gary J.
;   REGISTRATION NUMBER: 32,020
;   REFERENCE/DOCKET NUMBER: 2879-36
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (303) 863-9700
;     TELEFAX: (303) 863-0223
;     INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 208 amino acids
;         TYPE: amino acid
;         TOPOLOGY: linear
;       MOLECULE TYPE: protein
;   US-08-630-172-15

Query Match          100.0%;  Score 1149;  DB 5;  Length 288;
Best Local Similarity 100.0%;  Pred. No. 4 7e-113;
Matches 216;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 GLSHFCGSVTHVKVEVKEYATLSCGHNVSYEELAQTRIYQKEKKAVLTMMGDMNITPE 60
Db      27 GLSHFCGSVTHVKVEVKEYATLSCGHNVSYEELAQTRIYQKEKKAVLTMMGDMNITPE 86
Qy      61 YKNRTIDITNNLSIVILALRPSDGTYYECVVLKYERDAFKREHLAETVLSYKADFPPIPS 120
Db      87 YKRTIDITNNLSIVILALRPSDGTYYECVVLKYERDAFKREHLAETVLSYKADFPPIPS 146
Qy      121 ISDFEIPTSNIRRICSTSGGFPEPHISWLENGEELNAINTVSDPETYAVSSKLDF 180
Db      147 ISDFEIPTSNIRRICSTSGGFPEPHISWLENGEELNAINTVSDPETYAVSSKLDF 206
Qy      181 NMTTNHSFMCLIKYGHLYRNQTFNWNTTKQEHFPDN 216
Db      207 NMTTNHSFMCLIKYGHLYRNQTFNWNTTKQEHFPDN 242

RESULT 12
US-09-171-945-131
; Sequence 131, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
;   APPLICANT: Emery, Stephen
;   APPLICANT: Copley, Clive Graham
;   APPLICANT: Edge, Michael Derek
;   TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, and Their Therapeutic Use in an Adept System
;   FILE REFERENCE: Monoclonal Antibody to CEA
;   CURRENT APPLICATION NUMBER: US-09-171,945
;   CURRENT FILING DATE: 1998-10-29
;   PRIOR APPLICATION NUMBER: GB9703103-3
;   PRIOR FILING DATE: 1997-02-14
;   PRIOR APPLICATION NUMBER: GB9609405-7
;   PRIOR FILING DATE: 1996-05-04
;   PRIOR APPLICATION NUMBER: PCT/GB97/01165
;   PRIOR FILING DATE: 1997-04-29
;   NUMBER OF SEQ ID NOS: 131
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 131

Query Match          100.0%;  Score 1050;  DB 3;  Length 208;
Best Local Similarity 95.78%;  Pred. No. 7.6e-103;
Matches 199;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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QY 9 VIHTKEVATLSCGHNSVVEELAQTRIYWOKEKKMVLTMMSGDMNIWPEYKNRTIFD 68  
 1 Db 1 VIHTKEVATLSCGHNSVVEELAQTRIYWOKEKKMVLTMMSGDMNIWPEYKNRTIFD 60

QY 69 ITNNLSIVITALRPSDEGTYECVVLKYKEDAFKREHLAETVLTSYKADFPPTSIDFEIPT 128  
 1 Db 61 ITNNKSIVITALRPSDEGTYECVVLKYKEDAFKREHLAETVLTSYKADFPPTSIDFEIPT 120

QY 129 SNIRRLICSTSGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDFNMNTTNHSF 188  
 1 Db 121 SNIRRLICSTSGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDFNMNTTNHSF 180

QY 189 MCLIKVGHLRVNQTFNWNTTKQEHFPDN 216  
 1 Db 181 MCLIKVGHLRVNQTFNWNTTKQEHFPDN 208

RESULT 15  
 US -08-205-697A-17  
 ; Sequence 17, Application US/08205597A

QY 144 US-09-375-419-15  
 ; Sequence 15, Application US/09375419

GENERAL INFORMATION:  
 APPLICANT: Steitz, Uwe  
 TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
 TITLE OF INVENTION: LYMPHOCYTE VETO  
 NUMBER OF SEQUENCES: 41  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sheridan Ross & McIntosh  
 STREET: 1700 Lincoln Street, 35th Floor  
 CITY: Denver  
 STATE: Colorado  
 COUNTRY: U.S.  
 ZIP: 80203  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/375,419  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/630,172  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Connell, Gary J.  
 REGISTRATION NUMBER: 32,020  
 REFERENCE/DOCKET NUMBER: 2879-36  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 863-9700  
 TELEFAX: (303) 863-0223  
 INFORMATION FOR SEQ ID NO: 15:  
 LENGTH: 208 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Query Match 91.4%; Score 1050; DB 4; Length 208;  
 Best Local Similarity 95.7%; Pred. No. 7.6e-103;  
 Matches 1; Mismatches 8; Indels 0; Gaps 0;

QY 9 VIHTKEVATLSCGHNSVVEELAQTRIYWOKEKKMVLTMMSGDMNIWPEYKNRTIFD 68  
 1 Db 1 VIHTKEVATLSCGHNSVVEELAQTRIYWOKEKKMVLTMMSGDMNIWPEYKNRTIFD 60

QY 69 ITNNLSIVITALRPSDEGTYECVVLKYKEDAFKREHLAETVLTSYKADFPPTSIDFEIPT 128  
 1 Db 61 ITNNKSIVITALRPSDEGTYECVVLKYKEDAFKREHLAETVLTSYKADFPPTSIDFEIPT 120

RESULT 15  
 US -08-205-697A-17  
 ; Sequence 17, Application US/08205597A

GENERAL INFORMATION:  
 APPLICANT: Sharpe, Arlene H.  
 APPLICANT: Borriello, Francescopaolo  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadier, Lee M.  
 TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules  
 NUMBER OF SEQUENCES: 61  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE S COCKFIELD  
 STREET: 60 State Street, suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/205,697A  
 FILING DATE: 02-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragores, Any E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: BWI-120  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5941  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 306 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-205-697A-17

Query Match 48.8%; Score 561; DB 4; Length 306;  
 Best Local Similarity 50.7%; Pred. No. 4.3e-51;  
 Matches 41; Mismatches 58; Indels 2; Gaps 2;

QY 12 VTKEYEVATLSCGHNSVVEELAQTRIYWOKEKKMVLTMMSGDMNIWPEYKNRTIFDITN 71  
 1 Db 42 LSKSYRKDVLLPCRYSPHEDESDRTYQKHDKVYLSVTAGKLKWPEYKNRTLYDNT- 100

QY 72 NLSIVTALRPSDEGTYECVVLKYKEDAFKREHLAETVLTSYKADFPPTSIDFEIPTSN 131  
 1 Db 101 TYSILIGLVLSDRGTYSCVYQKERGTYEVKHALVKLSIKADFPPTSIDFEIPTNSGP SADT 160

QY 132 RRIICSTSGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDFNMNTTNHSFMCL 191  
 1 Db 161 KRICFASGGFPKRFWSLNGRELPGINTTISQDSELYTISQDFTNTTRNTHIKCL 220

QY 192 IKYGHLRVNQTFNWNTTKQEHFPDN 216  
 1 Db 221 IKYGAHVSEDFTEWKPPEDP-PDS 244

Search completed: April 24, 2002, 15:30:40  
Job time: 271 sec